

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2003, 23:28:26 : Search time 659 Seconds
(without alignments)
8159.758 Million cell updates/sec

Title: US-09-973-382C-1
Perfect score: 1992
Sequence: 1 agcaataactactaccacac.....taaaaaaaaaaaaaaaaaa 1992

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_19JUN03:*

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	1992	21	AAC61762
2	1702.6	85.5	2653	15	AAQ65520
3	1702.6	85.5	2653	24	ABX03677
4	1702.6	85.5	2653	24	ABK86204
5	1702.6	85.5	2653	24	ABK64556
6	1702.6	85.5	2653	24	ABL63670
7	1702.6	85.5	2653	25	ABQ83845
8	1702.6	85.5	2884	23	ABV22873

9	1702.6	85.5	2884	23	ABV23013
10	1702.6	85.5	2884	23	ABV28703
11	1702.6	85.5	2884	23	ABV28849
12	1690	84.8	2654	17	AACT36785
13	1687.2	84.7	2558	22	AACT78599
14	1687.2	84.7	2558	22	AAAS45976
15	1687.2	84.7	2558	25	ACAS47734
16	1687.2	84.7	2558	25	ABX982004
17	1687.2	84.7	2558	25	ABX984706
18	1687.2	84.7	2558	25	ACR05751
19	1687.2	84.7	2558	25	ABX92786
20	1687.2	84.7	2558	25	ABX97795
21	1687.2	84.7	2558	25	ABX78579
22	1687.2	84.7	2558	25	ABX75592
23	1687.2	84.7	2558	25	ABX76797
24	1687.2	84.7	2558	25	ABX16637
25	1584	79.5	2253	21	AAA09454
26	1584	79.5	2253	21	AAAD43985
27	1582.2	79.4	2226	21	AAAI2732
28	1412.4	70.9	2061	24	AAAD34009
29	1246.2	62.6	2082	21	AAA09459
30	1246.2	62.6	2256	21	AAA09458
31	981.8	49.3	1037	21	AAFI5651
32	885.4	44.4	3171	22	AAE93781
33	883.8	44.4	3110	21	AAZ58312
34	883.8	44.4	3771	22	AAH98667
35	557	28.0	656	21	AAFI5621
36	485.8	24.4	578	23	ABV43616
37	411	20.6	437	22	ABAS4719
38	411	20.6	437	22	AAK03001
39	411	20.6	437	23	ABS28047
40	400	20.1	442	24	ABK64577
41	348.6	17.5	435	23	ABV43871
42	238.8	12.0	308	23	ABV13812
43	238.8	12.0	455	23	ABV35023
44	231.4	11.6	486	23	ABV48264
45	226.8	11.4	309	23	ABV13650

ALIGNMENTS

RESULT 1	
AAC61762	
ID	AAC61762 standard; cDNA: 1992 BP.
XX	
AC	AAC61762;
XX	
DT	06-MAR-2001 (first entry)
XX	
DE	cDNA encoding a prostate-specific membrane antigen-like protein.
XX	
KW	Human; prostate specific membrane antigen like protein; cancer;
KW	PSMA-like protein; chromosome 11q14.3; schizophrenia;
KW	schizophrenia disorder type II locus; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS 527..1855
FT	/*tag= a
FT	/product= "prostate-specific membrane antigen-like protein"
XX	
PN	WO200061605-A1.
XX	
PD	19-OCT-2000.
XX	
PF	07-APR-2000; 2000MO-US09417.
XX	
PR	09-APR-1999; 99US-0128839.
XX	
PA	(SLOK) SLOAN KETTERING INST CANCER RES.

xx Heston MDW, O'Keefe DS:
xx WPI: 2000-679461/66.
DR P-PSDB: AAB19377.
xx
PT New DNA fragment encoding mammalian prostate specific membrane antigen
PT (PSMA) like protein, useful for distinguishing mammalian PSMA gene
PT expression or protein from PSMA-like gene expression or protein
xx
PS Claim 2; Page 56-57; 75pp; English.
xx
xx The present sequence encodes a human prostate specific membrane
CC antigen (PSMA) like protein. The PSMA-like gene is mapped to chromosome
CC 11q14.3, to the schizophrenia disorder type II locus. Antibodies
CC directed against PSMA-like protein are useful for diagnosing cancers
CC (prostate, bladder, pancreatic, sarcoma, melanoma, lung or kidney) or
CC neurological disorders such as schizophrenia. They may also be used
CC for screening for ligands of PSMA-like protein and imaging cells
CC expressing PSMA-like protein.
xx
SQ Sequence 1992 BP; 638 A; 352 C; 451 G; 551 T; 0 other:

Query Match 100.0%; Score 1992; DB 21; Length 1992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCAATCTCTACATACCAATTAAGACATTTCCAAATCTGATGTTGAGATTTTGA 60
DB 1 AGCAATCTCTACATACCAATTAAGACATTTCCAAATCTGATGTTGAGATTTTGA 60
OY 61 GAGCTTATAGTAGCAAAAAAGAAATTCCTCTGAGATGCTTTTGTAGGCC 120
DB 61 GAGCTTATAGTAGCAAAAAAGAAATTCCTCTGAGATGCTTTTGTAGGCC 120
OY 121 TAATGACAAAAGTTGAAGATTAAGTTCTAGTACTATTAAAGTAAATTTGAAAATG 180
DB 121 TAATGACAAAAGTTGAAGATTAAGTTCTAGTACTATTAAAGTAAATTTGAAAATG 180
OY 181 ATATTACCAATCTGGAACAACAATTTAAATTAAGAAAGAAAGACACTGTGTTTCTA 240
DB 181 ATATTACCAATCTGGAACAACAATTTAAATTAAGAAAGAAAGACACTGTGTTTCTA 240
OY 241 GGTAAAAATGCCAGCTGSCAGGGGGCCAAAGAGTCTTCTACTCAGACCCGTGTA 300
DB 241 GGTAAAAATGCCAGCTGSCAGGGGGCCAAAGAGTCTTCTACTCAGACCCGTGTA 300
OY 301 CTACTTGTCTCTGGGGTGAAGTCTCTATCCAGAGCTTGAATCTTCTGAGAGTGTGT 360
DB 301 CTACTTGTCTCTGGGGTGAAGTCTCTATCCAGAGCTTGAATCTTCTGAGAGTGTGT 360
OY 361 CCAGCGTGAATATCTCTAAATCTGAATGTGTCAGAGAGACCTCTCAGACAGGTACCC 420
DB 361 CCAGCGTGAATATCTCTAAATCTGAATGTGTCAGAGAGACCTCTCAGACAGGTACCC 420
OY 421 AGCAATGAATACGCTTATAGCATGAATTCAGAGGCTGTGGTCTTCCAAGTATTC 480
DB 421 AGCAATGAATACGCTTATAGCATGAATTCAGAGGCTGTGGTCTTCCAAGTATTC 480
OY 481 TGTTCATCCAGTGGATCTATGATGACAGAGCTCTAGAAAAAGGTTGCTCGC 540
DB 481 TGTTCATCCAGTGGATCTATGATGACAGAGCTCTAGAAAAAGGTTGCTCGC 540
OY 541 ACCACAGATAGCAGCTGAGAGAGAGCTCAAGTGTCTACAAATGTTGACCTGGCTT 600
DB 541 ACCACAGATAGCAGCTGAGAGAGAGCTCAAGTGTCTACAAATGTTGACCTGGCTT 600
OY 601 TACTGGAACCTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTAC 660
DB 601 TACTGGAACCTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTAC 660
OY 661 GAGATTTTACAAATGTGATGATCTCTCAGAGAGAGCACTGACACAGATATGTTCAT 720
DB 661 GAGATTTTACAAATGTGATGATCTCTCAGAGAGAGCACTGACACAGATATGTTCAT 720

DB 661 GAGATTTTACAAATGTGATGATCTCTCAGAGAGAGCACTGACACAGATATGTTCAT 720
OY 721 TCTGGAGAGTACCGGGACCTCATGAGTGTGTTGATTTGATTCACCTCAGAGTGAAGCAGC 780
DB 721 TCTGGAGAGTACCGGGACCTCATGAGTGTGTTGATTTGATTTGATTCACCTCAGAGTGAAGCAGC 780
OY 781 TGTGTTTCATGAACCTGTGAGAGCTTTGGAACACTGAAAAAGAGAGGTGAGACCTAG 840
DB 781 TGTGTTTCATGAACCTGTGAGAGCTTTGGAACACTGAAAAAGAGAGGTGAGACCTAG 840
OY 841 AAGAACATTTTGTTCGCAACCTGGGATGCGAAGAAATTTGCTTCTGCTCTACTGA 900
DB 841 AAGAACATTTTGTTCGCAACCTGGGATGCGAAGAAATTTGCTTCTGCTCTACTGA 900
OY 841 AAGAACATTTTGTTCGCAACCTGGGATGCGAAGAAATTTGCTTCTGCTCTACTGA 900
DB 841 AAGAACATTTTGTTCGCAACCTGGGATGCGAAGAAATTTGCTTCTGCTCTACTGA 900
OY 901 GTGGGAGAGATTAATCAAGACTCTTCAAGACGCGGTGCTATATTAATGCTGA 960
DB 901 GTGGGAGAGATTAATCAAGACTCTTCAAGACGCGGTGCTATATTAATGCTGA 960
OY 961 CTGATCTATAGAGAAAGAACTACACTGAGAGTTGATTTGATACACCACTGATGTACAGCTT 1020
DB 961 CTGATCTATAGAGAAAGAACTACACTGAGAGTTGATTTGATACACCACTGATGTACAGCTT 1020
OY 1021 GGTATACAACTAACAAAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAAGCAAACTCT 1080
DB 1021 GGTATACAACTAACAAAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAAGCAAACTCT 1080
OY 1081 TTATGAAGTTGAGCTAAAAAAGTCCCTCCAGAGTCAAGTGCATGCGCAGATAG 1140
DB 1081 TTATGAAGTTGAGCTAAAAAAGTCCCTCCAGAGTCAAGTGCATGCGCAGATAG 1140
OY 1141 CAAATTTGGGATCTGGAATGATTTTGAAGTGTCTTCCAAACGACTTGAATGTGCTAG 1200
DB 1141 CAAATTTGGGATCTGGAATGATTTTGAAGTGTCTTCCAAACGACTTGAATGTGCTAG 1200
OY 1201 CAGAGCAAGGATCTAAAAATTTGGGAAACAAATTCAGAGGCTATCCAGCTATCA 1260
DB 1201 CAGAGCAAGGATCTAAAAATTTGGGAAACAAATTCAGAGGCTATCCAGCTATCA 1260
OY 1261 CAGTGTCTATGAACATATGATGATGTTGGAAGAAATTTATGATCCAAATGTTTAAATATCA 1320
DB 1261 CAGTGTCTATGAACATATGATGATGTTGGAAGAAATTTATGATCCAAATGTTTAAATATCA 1320
OY 1321 CCTCAGTGTGCCCCAGGTTGAGAGAGGATGTTTGTAGCTTACCAATTCATAGTGTCT 1380
DB 1321 CCTCAGTGTGCCCCAGGTTGAGAGAGGATGTTTGTAGCTTACCAATTCATAGTGTCT 1380
OY 1381 CCTTTGATTTGTCGAGATTAATGCTGTAGTTTAAAGAAAGTATCTGCAAAATCTCAAA 1440
DB 1381 CCTTTGATTTGTCGAGATTAATGCTGTAGTTTAAAGAAAGTATCTGCAAAATCTCAAA 1440
OY 1441 TATTTCTATGAACATCCACAGAAATGAAGACATAGTTTATCATTTGATTCACCTTT 1500
DB 1441 TATTTCTATGAACATCCACAGAAATGAAGACATAGTTTATCATTTGATTCACCTTT 1500
OY 1501 TTTCTGAGTAAAAATTTTACAGAAATTTGCTTCCAAGTTACAGGAGAGACTCCAGGACTT 1560
DB 1501 TTTCTGAGTAAAAATTTTACAGAAATTTGCTTCCAAGTTACAGGAGAGACTCCAGGACTT 1560
OY 1561 TGACAAAAGCAACCAATATTTGTAAGATGATCAATCAATCAATGTTTTCGGAAG 1620
DB 1561 TGACAAAAGCAACCAATATTTGTAAGATGATCAATCAATCAATGTTTTCGGAAG 1620
OY 1621 AGCATTTTATGATCCATTAGAGGTTACAGAGACCTTTTATATAGGATGTCATCTATGC 1680
DB 1621 AGCATTTTATGATCCATTAGAGGTTACAGAGACCTTTTATATAGGATGTCATCTATGC 1680
OY 1681 TCCAGAGAGCCACACAAAGTATGCGAGGAGTCAATTCACAGAAATTTATATGATGCTGT 1740
DB 1681 TCCAGAGAGCCACACAAAGTATGCGAGGAGTCAATTCACAGAAATTTATATGATGCTGT 1740
OY 1741 TGATATTTGAAGCAAAATGAGACCTTCCAGAGCCTGGGAGATGTTGAAGAGACGATTC 1800
DB 1741 TGATATTTGAAGCAAAATGAGACCTTCCAGAGCCTGGGAGATGTTGAAGAGACGATTC 1800

Oy		1801	TGTTGCAGCCCTTCAACAGCGCAGCGAGCGAGACTTGATGTGAAGTAGCCTAAGACGA	1866
Dd		1801	TGTTGCAGCCCTTCACAGCGCAGCGAGCGAGACTTGATGTGAAGTAGCCTAAGACGA	1860
Oy		1861	TTCTTTGAGACCTCTGTATTGTAATTTGGTGTATGTCACATCAAAGAATAATAATGGSTA	1920
Dd		1861	TTCTTTGAGACCTCTGTATTGTAATTTGGTGTATGTCACATCAAAGAATAATAATGGSTA	1920
Oy		1921	TATTGATPAATTTTTAAAAATTCGTATATTGTAATPAAGTGAATATTATATATAAAAAA	1980
Dd		1921	TATTGATPAATTTTTAAAAATTCGTATATTGTAATPAAGTGAATATTATATATAAAAAA	1980
Oy		1981	AAAAAAAAAAAAA 1992	
Dd		1981	AAAAAAAAAAAAA 1992	
<hr/>				
RESULT 2				
ID	AA065520	standard; cDNA; 2653 BP.		
XX	AA065520;			
XX	AC			
XX	DT	25-MAR-2003 (updated)		
DF	DT	11-JAN-1995 (first entry)		
XX				
DE		Prostate-specific membrane antigen cDNA.		
XX				
KW		Prostate-specific membrane antigen; PSM; prostate cancer;		
KW		transmembrane glycoprotein; imaging; targeting; tumour detection;		
XK		antibody detection; ds.		
OS		Homo sapiens.		
XX				
FH	Key	Location/Qualifiers		
FT	CDS	262..2514		
FT		/*tag= a		
FT		/product= prostate specific membrane antigen (PSM)		
XX				
PN	WO9409820-A1.			
XX				
PD	11-MAY-1994.			
XX				
PE	05-NOV-1993; 93WO-US10624.			
XX				
PR	05-NOV-1992; 92US-0973337.			
XX				
PA	(SLOK) SLOAN KETTERING INST CANCER.			
XX				
PI	Fair WR, Heston MDW, Israeli RS;			
XX				
DR	WPI; 1994-167129/20.			
XX	P-PSDB; AAR55097.			
PT		Prostate-specific membrane antigen and DNA encoding it - is		
PT		useful for detecting haematogenous micro-metastatic tumour cells		
PT		and for identifying ligands which bind to PSM Ag		
XX				
PS	Claim 3; Page 103-106; 196pp; English.			
XX				
CC	AA065520 encodes a prostate specific membrane antigen (PSM, AAR55097).			
CC	The PSM coding sequence is useful for suppressing or modulating the			
CC	metastatic ability of prostate tumour cells to grow, or for			
CC	eliminating them. The protein is useful to identify or purify ligands			
CC	of the Ag. It is also an attractive target for Ab-directed imaging			
CC	and targeting of prostatic tumour deposits.			
CC	(Updated on 25-MAR-2003 to correct PN field.)			
XX				
SQ	Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other:			
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Query Match	85.5%; Score 1702.6; DB 15; Length 2653;			
Best Local Similarity	98.5%; Pred. No. 0;			

	Matches	1729	Conservative	0	Mismatches	24	Indels	2	Gaps	1
QY	240	AGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGCATATTCCTACTCAGACCTGCTG	299							
Db	899	AGGTTAAAAAATGCCAGCTGGCAGGGGCCAAAGGATTCCTACTCCAGACCTGCTG	958							
QY	300	ACTACTTTCCTCCCTGGGTGGAAGTCCATCCAGACGGTTGGAAATTCCTCTGGAGTGGTG	359							
Db	959	ACTACTTTCCTCCCTGGGTGGAAGTCCATCCAGATGGTTGGAAATTCCTCTGGAGTGGTG	1018							
QY	350	TCACGCGTGAAGAAATCCCTAAATCTGAATGGTGCAGAGACCCCTCTCACACAGTTTAC	419							
Db	1019	TCACGCGTGAAGAAATCCCTAAATCTGAATGGTGCAGAGACCCCTCTCACACAGTTTAC	1078							
QY	420	CAGCAAAATGATAGCGCTTATATAGGCATGGAAATTCGACAGGCTGTGGTTCTTCCAAAGTATC	479							
Db	1079	CAGCAAAATGAAATATGCTTATATAGCGCTGAAGATTCGACAGGCTGTGGTTCTTCCAAAGTATC	1138							
QY	480	CTGTTCATCCAGTTGGATGATATGATGTGACAGAAAGCTCTCTAGAAAAATATGGGTGGCTCAG	539							
Db	1139	CTGTTCATCCAGTTGGATGATATGATGTGACAGAAAGCTCTCTAGAAAAATATGGGTGGCTCAG	1199							
QY	540	CACCAACAGATAGCAGCTGAGAGAGAGTCTCAAAGTGTCTCTACATGTTGACCTGGCT	599							
Db	1199	CACCAACCGAATAGCAGCTGAGAGAGAGATCTCAAAGTGTCTCTACATGTTGACCTGGCT	1258							
QY	600	TTACTGGAAACCTTTTCTACAAAAAGTCAAAAGATGCACATCCACTCCTACCAATGAAGTGA	659							
Db	1259	TTACTGGAAACCTTTTCTACAAAAAGTCAAAAGATGCACATCCACTCCTACCAATGAAGTGA	1318							
QY	660	CGAGAAATTTACAAATGTGATAGTACTCTCAGAGAGACAGTGGAAACACACAGATATGTCA	719							
Db	1319	CAAGAAATTTACAAATGTGATAGTACTCTCAGAGAGACAGTGGAAACACACAGATATGTCA	1378							
QY	720	TTCTGGGAGGTTCACCCGGACCTCATGGGTGTGGTGGTATTTAGCCCTCAAGTGGAGACAG	779							
Db	1379	TTCTGGGAGGTTCACCCGGACCTCATGGGTGTGGTGGTATTTAGCCCTCAAGTGGAGACAG	1438							
QY	780	CTGTGTTTCATGAAGAACTGTGAGAGACCTTGGAAACCTAAAGAAAGGAGGTGGAGACCTA	839							
Db	1439	CTGTGTTTCATGAAGAAATTTGTGAGAGACCTTGGAAACCTAAAGAAAGGAGGTGGAGACCTA	1499							
QY	840	GAAGAACAAATTTGTTGCCAAGCTGGGATGCAGAGAAATTTGGTCTCTTGCTACTG	899							
Db	1499	GAAGAACAAATTTGTTGCCAAGCTGGGATGCAGAGAAATTTGGTCTCTTGCTACTG	1558							
QY	900	AGTGGGCGAGAGATATATCAAGACCTCTCAAGAGCGTGGGTGGCTATTTAATGCTG	959							
Db	1559	AGTGGGCGAGAGAGATATCAAGACCTCTCAAGAGCGTGGGTGGCTATTTAATGCTG	1618							
QY	960	ACTCATCTATAGAAAGGAAACTACACTGTGAGAGTTGATTTGTACACACACTGATGTACACT	1019							
Db	1619	ACTCATCTATAGAAAGGAAACTACACTGTGAGAGTTGATTTGTACACACCGCTGATGTACACT	1678							
QY	1020	TGATATACAACTTAACAAAGAGCGTGAAGACCCCGATGAGGCTTTGAAGCAAAATCTC	1079							
Db	1679	TGATATACAACTTAACAAAGAGCGTGAAGACCCCGATGAGAGGCTTTGAAGCAAAATCTC	1738							
QY	1080	TTTATGAAAGTTGGACATAAAAAAGTCCCTCCAGAGTTAGTGGCATGTCGCCAGAGATTA	1139							
Db	1739	TTTATGAAAGTTGGACATAAAAAAGTCTCTCCAGAGTTAGTGGCATGTCGCCAGAGATTA	1798							
QY	1140	GCAAAATTTGGATCTGGGAAATGATTTTGAAGTGTCTTCAACGACATTTGGAATTTGCTTCAG	1199							
Db	1799	GCAAAATTTGGATCTGGGAAATGATTTTGAAGTGTCTTCAACGACATTTGGAATTTGCTTCAG	1858							
QY	1200	GCAGAGCAGCGTATATCTATTAATAATTGGGAAACAAACAAATTTAGGGGCTATCCACTGTATC	1259							
Db	1859	GCAGAGCAGCGTATATCTATTAATAATTGGGAAACAAACAAATTTAGGGGCTATCCACTGTATC	1918							
QY	1260	ACAAGTCTATGAAGAAATATGATGTTGGTGAAGAAAGTTTATGATCCAATGTTTAAATATC	1319							
Db	1919	ACAAGTCTATGAAGAAATATGATGTTGGTGAAGAAAGTTTATGATCCAATGTTTAAATATC	1978							

QY	1320	ACCTCAGCTGCGCCAGGTTGAGAGAGGATGGTTTGACCTGACCAATTCCATPAGTC	1379
Db	1979	ACCTCAGCTGCGCCAGGTTGAGAGAGGATGGTTTGACCTGACCAATTCCATPAGTC	2038
QY	1380	TCCCTTTTGATGTGCGAATTTATGCTGAGTTTAAAGAAATGATGACCAAAATCTACA	1439
Db	2039	TCCCTTTTGATGTGCGAATTTATGCTGAGTTTAAAGAAATGATGACCAAAATCTACA	2098
QY	1440	ATATTTTCTATGAACATCTCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTT	1499
Db	2099	GTAATTTCTATGAACATCTCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTT	2158
QY	1500	TTTTCGACGTAAAAAATTTTACAGAAATTTGCTTCCAAAGTTAGGAGAGACTCCAGAGCT	1559
Db	2159	TTTTCGACGTAAAAAATTTTACAGAAATTTGCTTCCAAAGTTAGGAGAGACTCCAGAGCT	2218
QY	1560	TTGCAAAAAGCAACCCCAATATTTGTAAGAAATGATGAATGATCAACTCATGTTCTGAAA	1619
Db	2219	TTGCAAAAAGCAACCCCAATATTTGTAAGAAATGATGAATGATCAACTCATGTTCTGAAA	2278
QY	1620	GAGCATTTATGATCCATTAGGCTTTACACAGAACCTTTTATAGCATGTCTATATG	1679
Db	2279	GAGCATTTATGATCCATTAGGCTTTACACAGAACCTTTTATAGCATGTCTATATG	2338
QY	1680	CTCCAGAGCAGCCACAAACAGATATCAGGAGAGTATTCGCCAGAAATTTATGATCTCTGT	1739
Db	2339	CTCCAGAGCAGCCACAAACAGATATCAGGAGAGTATTCGCCAGAAATTTATGATCTCTGT	2398
QY	1740	TTGATATTTGAAGCAAAAGTGGAGCCCTTCCAAAGCCTTGCGGAGATGTGAAGACAGATTT	1799
Db	2399	TTGATATTTGAAGCAAAAGTGGAGCCCTTCCAAAGCCTTGCGGAGATGTGAAGACAGATTT	2458
QY	1800	CTGTGTGACGCTTACAGTGTGACGAGCTGTGAGAGACTTTAGAGAACTACCTTAAGAGC	1859
Db	2459	ATGTTTGCAGCCTTACAGTGTGACGAGCTGTGAGAGACTTTAGAGAACTACCTTAAGAGC	2518
QY	1860	ATTCTTTTGAAGACTCTGTATTTGATTTGTGTGTATGCTACTC--AAAAGATATTAATGG	1917
Db	2519	ATTCTTTTGAAGAAATCCGATTTGATTTGTGTGTATGCTACTCAGAAAAGATTCGTAATGG	2578
QY	1918	GTAATATTTGATTAATTTTAAATTTGTAATTTGTAATTAAGTTGAATATTTATATATATAA	1977
Db	2579	GTAATATTTGATTAATTTTAAATTTGTAATTTGTAATTAAGTTGAATATTTATATATATAA	2638
QY	1978	AAAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAAA 2653	
RESULT 3			
ABX03677			
ID	ABX03677	standard; DNA; 2653 BP.	
XX	ABX03677;		
AC			
XX			
DT	08-JAN-2003	(first entry)	
XX			
DE	DNA encoding folate hydrolase (prostate specific membrane antigen) 1.		
XX			
KW	Cell-mediated immunity; cellular immune response; CTL response;		
KW	tumour neovasculation; anti-angiogenesis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200269907-A2.		
PD	12-SEP-2002.		
XX			
PF	07-MAR-2002; 2002WO-US07204.		
XX			
XX	07-MAR-2001; 2001US-274063P.		

Query Match	Best Local Similarity	85.5%;	Score 1702.6;	DB 24;	Length 2653;
Matches 1729;	Conservative	0;	Mismatches 24;	Indels 2;	Gaps 1;
QY	240	AGGTTAAAAATGCCCAGCTGGACAGGCGCCAAAGAGATCTTCTACTAGACCCCTG	299		
DB	899	AGGTTAAAAATGCCCACTGGACAGGCGCCAAAGAGATCTTCTACTAGACCCCTG	958		
QY	300	ACTACTTGGCTCCTGGGGTGAAGTCCATCCAGAGCGTTGGAATCTTCTGGAGGTGG	359		
DB	959	ACTACTTGGCTCCTGGGGTGAAGTCCATCCAGAGCGTTGGAATCTTCTGGAGGTGG	1018		
QY	360	TTCAGCGGTGGAATATCTTAAATCTGATGATGGTGAGGAGACCCCTCACACGAGTTAC	419		
DB	1019	TTCAGCGGTGGAATATCTTAAATCTGATGATGGTGAGGAGACCCCTCACACGAGTTAC	1078		
QY	420	CAGCAAAATGATAGCGCTTATAGCGATGGAATTCGACAGGCGTGTGGCTTCCAGATATC	479		
DB	1079	CAGCAAAATGATAGCGCTTATAGCGCGTGAATTCGACAGGCGTGTGGCTTCCAGATATC	1138		
QY	480	CTGTTTCATCCAGTTGGATCTATGATGACACAGAAAGCTCTTAGAAAAATGGGTGGCTAG	539		
DB	1139	CTGTTTCATCCAGTTGGATCTATGATGATGACACAGAAAGCTCTTAGAAAAATGGGTGGCTAG	1198		
QY	540	CACACACAGATAGAGCTGGAGAGAGAGTCCTCAAGTGTCTTCAATGTTGAGACTGGCT	599		
DB	1199	CACACACAGATAGAGCTGGAGAGAGAGTCCTCAAGTGTCTTCAATGTTGAGACTGGCT	1258		
QY	600	TTACTGGAATCTTTCTACACAAAAGTCAAGATGCACATCCACTCTTACCAATGAAGTGA	659		
DB	1259	TTACTGGAATCTTTCTACACAAAAGTCAAGATGCACATCCACTCTTACCAATGAAGTGA	1318		
QY	660	CGAGAAATTTCAATGATAGTATAGTATCTTCAGAGAGAGAGTGAACCGACAGATATGTCA	719		
DB	1319	CGAGAAATTTCAATGATAGTATAGTATCTTCAGAGAGAGAGTGAACCGACAGATATGTCA	1378		
QY	720	TTCGAGAGATGCACCGGAGCTCATGAGGTGTTGGTGTATTTGACCCCTCAGAGTGGAGAC	779		
DB	1379	TTCGAGAGATGCACCGGAGCTCATGAGGTGTTGGTGTATTTGACCCCTCAGAGTGGAGAC	1438		
QY	780	CTGTGTTTCATGAATCTGTAGAGAGCTTTGGAACACTGAAAAAGAAAGGTGGAGACTTA	839		
DB	1439	CTGTGTTTCATGAATCTGTAGAGAGCTTTGGAACACTGAAAAAGAAAGGTGGAGACTTA	1498		

QY 840 GAAGAACAAATTTGTTGCAAGCTGGGATGCAGAAATTTGGCTCTCTGTTCTACTG 899
 DB 1499 GAAGAACAAATTTGTTGCAAGCTGGGATGCAGAAATTTGGCTCTCTGTTCTACTG 1558
 QY 900 AGTGGCAGAGGATTAATTCAGAGCTCTCCAGAGCGTGGCTGGCTTATATTAAATGCTG 959
 DB 1559 AGTGGCAGAGGATTAATTCAGAGCTCTCCAGAGCGTGGCTGGCTTATATTAAATGCTG 1618
 QY 960 ACTCATCTATAGAGGAACTACACTCTGAGATTTGATTTGATACACATGATGTACAGCT 1019
 DB 1619 ACTCATCTATAGAGGAACTACACTCTGAGATTTGATTTGATACACATGATGTACAGCT 1678
 QY 1020 TGGTATACCAACCTAAACAAAGAGCTTAAAGAGCTTGAAGAGCTTGAAGAGCTTGA 1079
 DB 1679 TGGTATACCAACCTAAACAAAGAGCTTAAAGAGCTTGAAGAGCTTGAAGAGCTTGA 1738
 QY 1080 TTTATGAAAGTTGGACTTAAAGAAAGTCTCCAGAGTTCACTGGCATGCCAGATTA 1139
 DB 1739 TTTATGAAAGTTGGACTTAAAGAAAGTCTCCAGAGTTCACTGGCATGCCAGATTA 1798
 QY 1140 GCAAAATTTGGGATCTGGAATGATTTGAGGTGTTCTTCCAGAGCTTGAATTTGCTCAG 1199
 DB 1799 GCAAAATTTGGGATCTGGAATGATTTGAGGTGTTCTTCCAGAGCTTGAATTTGCTCAG 1858
 QY 1200 GCAGACGACGATTAATTAATAAATTTGGGAAACAAACAAATTCAGCGCTATCCAGTATC 1259
 DB 1859 GCAGACGACGATTAATTAATAAATTTGGGAAACAAACAAATTCAGCGCTATCCAGTATC 1918
 QY 1260 ACAGTCTATAGAAACATATGAGTGTGGGAAAGTTTATGATCCAAATGTTTAAATATC 1319
 DB 1919 ACAGTCTATAGAAACATATGAGTGTGGGAAAGTTTATGATCCAAATGTTTAAATATC 1978
 QY 1320 ACCCTACGTGGGCCAGGTTCCAGAGGAGTGGTGTGTTGAGCTAGCCATTCATATGTCG 1379
 DB 1979 ACCCTACGTGGGCCAGGTTCCAGAGGAGTGGTGTGTTGAGCTAGCCATTCATATGTCG 2038
 QY 1380 TCCCTTTGATTTGTCAGATTAATGCTGATTTTAAGAAAGTATGCTGAACAAATCTACA 1439
 DB 2039 TCCCTTTGATTTGTCAGATTAATGCTGATTTTAAGAAAGTATGCTGAACAAATCTACA 2098
 QY 1440 AATATTTCTATGAACATCCACAGGAAATGAGACATACAGTTATCATTTGATTCCTTT 1499
 DB 2099 GATATTTCTATGAACATCCACAGGAAATGAGACATACAGTTATCATTTGATTCCTTT 2158
 QY 1500 TTTTCGACATTAATAATTTTACAGAAATGCTTCCAGTTCCAGCCGAGAGCTCAGAGCT 1559
 DB 2159 TTTTCGACATTAATAATTTTACAGAAATGCTTCCAGTTCCAGTTCCAGAGCTCAGAGCT 2218
 QY 1560 TTGACAAAAGCAACCAATATTTGTTAAGATGATGAATGATCAACTCATTTCTGGAAA 1619
 DB 2219 TTGACAAAAGCAACCAATATTTGTTAAGATGATGAATGATCAACTCATTTCTGGAAA 2278
 QY 1620 GAGCATTTATGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATATG 1679
 DB 2279 GAGCATTTATGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATATG 2338
 QY 1680 CTCACAGCAGCCACAAACAGTATGCGAGGGAGTCATTTCCAGGAATTTATGATGCTCTGT 1739
 DB 2339 CTCACAGCAGCCACAAACAGTATGCGAGGGAGTCATTTCCAGGAATTTATGATGCTCTGT 2398
 QY 1740 TTGATTTGAAAGCAAAAGTGAGACCTTCCAGAGCCCTGGGAGATGGAAGAGACATTTT 1799
 DB 2399 TTGATTTGAAAGCAAAAGTGAGACCTTCCAGAGCCCTGGGAGATGGAAGAGACATTTT 2458
 QY 1800 CTGTTGACGCTTCCACAGTGCAGGAGCTGCAAGAGACTTTGAGTGAAGTATGCTTAAGAG 1859
 DB 2459 ATGTTGACGCTTCCACAGTGCAGGAGCTGCAAGAGACTTTGAGTGAAGTATGCTTAAGAG 2518
 QY 1860 ATTCTTAGAGACTGTTGATTAATTTGTTGATGATGTCATC - -AAAATAATTAATG 1917
 DB 2519 ATTCTTAGAGACTGTTGATTAATTTGTTGATGATGTCATCAGAAAAGAAATCTGTAATG 2578

QY 1918 GTATATTGATTAATTTTAAATTTGATATATTGAATTAAGTGAATATTATATATAAA 1977
 DB 2579 GTATATTGATTAATTTTAAATTTGATATATTGAATTAAGTGAATATTATATATAAA 2638
 QY 1978 AAAAAAAAAAAAAA 1992
 DB 2639 AAAAAAAAAAAAAA 2653

RESULT 4
 ABK86204
 ID ABK86204 standard; cDNA; 2653 BP.
 XX
 AC ABK86204;
 XX
 DF 24-SEP-2002 (first entry)
 XX
 DE cDNA encoding human prostate specific membrane antigen (PSMA) variant.
 XX
 KW Human: prostate specific membrane antigen; PSMA; cytostatic; antiviral;
 KW immunostimulant; cell-mediated immune response; tumour; breast cancer;
 KW virus infection; prostate cancer; colorectal cancer; pancreatic cancer;
 KW lymphoma; leukaemia; hepatitis virus; lentivirus; herpesvirus;
 KW human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN key Location/Qualifiers
 FT CDS 262..2514
 FT /*tag= a
 FT /product= "Prostate specific membrane antigen (PSMA)
 variant with signal sequence deleted"
 XX
 PN WO200240059-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 01-NOV-2001; 2001MO-US45626.
 XX
 PR 01-NOV-2000; 2000US-0704232.
 XX
 PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
 PA (MNC/) MINCHEFF M S.
 PA (LOUK/) LOUKINOV D I.
 PA (ZOUB/) ZOUBAK S.
 XX
 PI Mincheff MS, Loukinov DI, Zoubak S;
 XX
 DR WPI: 2002-527524/56.
 DR P-PSDB; AUC98920.
 XX
 PT Inducing a cell-mediated immune response against a target antigen,
 PT reducing undesired cells and stimulating presentation of an antigen by
 PT a cell, comprises administering a polynucleotide encoding a variant of
 PT an antigen -
 XX
 PS Example 1; Page 114-118; 146pp; English.
 XX
 CC The invention relates to a method of inducing a cell-mediated immune
 CC response against a cell comprising a target antigen (I) in a subject,
 CC treating a subject having undesired cells, for example tumour cells,
 CC or virally infected cells (C), reducing the number of (C) in a subject,
 CC and stimulating presentation of (I) by a cell. This is done by
 CC administering a polynucleotide (II) encoding a variant of (I), so that
 CC (II) expressed in a cell and cell-mediated immune response is induced.
 CC The method can be used to treat prostate cancer, breast cancer,
 CC colorectal cancer and pancreatic cancer, as well as lymphomas and
 CC leukemias. The method is also useful in treating chronic viral
 CC infections such as those caused by hepatitis viruses, lentiviruses
 CC (including human immunodeficiency virus (HIV)), herpesviruses and the
 CC flaviviruses and pestiviruses. The present sequence represents the coding
 CC sequence of human prostate specific membrane antigen (PSMA) variant
 CC which has the signal sequence deleted, used as a target antigen in the

XX 07-AUG-2001; 2001MO-US24708.
XX 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX (GENE-) GENE LOGIC INC.
PA (NISB) JAPAN TOBACCO INC.
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX WPI: 2002-257476/30.
DR

Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PI detecting expression levels of one or more genes in prostate cells from
PI patient that are differentially regulated compared to normal prostate
PI cells

Disclosure; Page 265-266; 444pp; English.

XX The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK6106-ABK6860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX

Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;

Query Match 85.5%; Score 1702.6; DB 24; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0; Mismatches 24; Indels 2; Gaps 1;
Matches 1729; Conservative 0;

QY 240 AGGTTAAATGCCCCAGCTGGCAGAGGGCCAAAGAGTCAATCTCTACTCAGACCCCTGCTG 299
DB 899 AGGTTAAATGCCCCAGCTGGCAGAGGGCCAAAGAGTCAATCTCTACTCAGACCCCTGCTG 958
QY 300 ACTACTTTGCTCTCTGGGGTGAAGTCTTCCAGACGGTTGGAATCTTCTCTGGAGGTG 359
DB 959 ACTACTTTGCTCTCTGGGGTGAAGTCTTCCAGAGTGTGGATCTTCTCTGGAGGTG 1018
QY 360 TCCAGCTGGAAATATCTCTAAATCTGATGGTGCAGGAGACCTCTCACACAGGTTC 419
DB 1019 TCCAGCTGGAAATATCTCTAAATCTGATGGTGCAGGAGACCTCTCACACAGGTTC 1078
QY 420 CAGCAATGAATAGCCTTATAGGATGGAATTCAGAGGCTGTGGTCTTCCAAATATTC 479
DB 1079 CAGCAATGAATAGCCTTATAGGATGGAATTCAGAGGCTGTGGTCTTCCAAATATTC 1138
QY 480 CTGTTTCATCCAGTTGGATCTATGATGCACAGAGCTCTTGAAGAAAATGGTGGCTAG 539
DB 1139 CTGTTTCATCCAGTTGGATCTATGATGCACAGAGCTCTTGAAGAAAATGGTGGCTAG 1198
QY 540 CACCAACGATAGCAGCTGGAGAGGAATCTCAAGGTCTTCAAAATTTGGAGCTGCT 599
DB 1199 CACCAACGATAGCAGCTGGAGAGGAATCTTCAAAATTTGGAGCTGCT 1258

QY 600 TTACTGAAAGCTTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAAGTGA 659
DB 1259 TTACTGAAAGCTTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAAGTGA 1318
QY 660 CGAGAAATTTACAAATGTATAGTACTCTCAGAGAGCAGTGGAGACACAGATATGTCA 719
DB 1319 CAAGAAATTTACAAATGTATAGTACTCTCAGAGAGCAGTGGAGACACAGATATGTCA 1378
QY 720 TTCTGGAGAGTCACCGGAGCTCATGGGTTGGTGGTATGATGACCTTCAGATGGAGAG 779
DB 1379 TTCTGGAGAGTCACCGGAGCTCATGGGTTGGTGGTATGATGACCTTCAGATGGAGAG 1438
QY 780 CTGTTGTTCAATGAAGCTGTGAGAGCTTTGGAACCTGAAAAAGAGAGTGGAGACCTA 839
DB 1439 CTGTTGTTCAATGAAGCTGTGAGAGCTTTGGAACCTGAAAAAGAGAGTGGAGACCTA 1498
QY 840 GAGAACAAATTTTGTTCAGAGCTGGAGATGAGAGAAATTTGCTTCTGTTCTACTG 899
DB 1499 GAGAACAAATTTTGTTCAGAGCTGGAGATGAGAGAAATTTGCTTCTGTTCTACTG 1558
QY 900 AGTGGCAGAGGATTAATTCAGACCTCTCAAGACCGTGGCTGCTATATTAATGCTG 959
DB 1559 AGTGGCAGAGGATTAATTCAGACCTCTCAAGACCGTGGCTGCTATATTAATGCTG 1618
QY 960 ACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATGTACACACTGATGTACAGCT 1019
DB 1619 ACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATGTACACACTGATGTACAGCT 1678
QY 1020 TGGTTACACCTAACAAAGAGCTGAAAGCCCTGATGAAAGGCTTTAAGGCAATCTC 1079
DB 1679 TGGTTACACCTAACAAAGAGCTGAAAGCCCTGATGAAAGGCTTTAAGGCAATCTC 1138
QY 1080 TTTATGAAGTTGGCTAAAAAAGTCCCTCCCGAGCTTCAGTGGCAATGCCAGATTA 1139
DB 1739 TTTATGAAGTTGGCTAAAAAAGTCCCTCCCGAGCTTCAGTGGCAATGCCAGATTA 1198
QY 1140 GCAAAATTTGGATCTGAAATGATTTTGAAGTGTCTTCCACAGCTTGAATGCTTGA 1199
DB 1799 GCAAAATTTGGATCTGAAATGATTTTGAAGTGTCTTCCACAGCTTGAATGCTTGA 1858
QY 1200 GCAGAGCAGGATATCTAAAAATTTGGGAAACAAATTCACGGGCTATCCACTGTATC 1259
DB 1859 GCAGAGCAGGATATCTAAAAATTTGGGAAACAAATTCACGGGCTATCCACTGTATC 1918
QY 1260 ACAGTGTATGAAGAAATATGATGTTGGTGAAGAAATTTTATGATCCATGTTAAATATC 1319
DB 1919 ACAGTGTATGAAGAAATATGATGTTGGTGAAGAAATTTTATGATCCATGTTAAATATC 1978
QY 1320 ACCTCACTGTGGCCAGGTTGAGAGAGGATGTGTTGAGCTAGCCAAATTCATATGTC 1379
DB 1979 ACCTCACTGTGGCCAGGTTGAGAGAGGATGTGTTGAGCTAGCCAAATTCATATGTC 2038
QY 1380 TCCCTTTGATTTGCGAATTTATGTGTATGTTTAAAGAAATATGCTACAAATCTACA 1439
DB 2039 TCCCTTTGATTTGCGAATTTATGTGTATGTTTAAAGAAATATGCTACAAATCTACA 2098
QY 1440 AATTTCTATGAATACATCCAGAGAAATGAGACATACAGTTATCATTTGTTTACATTT 1499
DB 2099 GATTTCTATGAATACATCCAGAGAAATGAGACATACAGTTATCATTTGTTTACATTT 2158
QY 1500 TTTCTGCAAGTAAAAATTTTACAGAAATTTGTTCCAAATTCAGGAGAGACTCCAGACT 1559
DB 2159 TTTCTGCAAGTAAAAATTTTACAGAAATTTGTTCCAAATTCAGGAGAGACTCCAGACT 2218
QY 1560 TTGACAAAGCAACCAATATTTGTTAGAAATGATGATCAACTATGTTTCTGAAA 1619
DB 2219 TTGACAAAGCAACCAATATTTGTTAGAAATGATGATCAACTATGTTTCTGAAA 2278
QY 1620 GAGCATTTATGATCATTTAGAGTTTACAGACAGACCTTTTATAGGATTCATCATATG 1679
DB 2279 GAGCATTTATGATCATTTAGAGTTTACAGACAGACCTTTTATAGGATTCATCATATG 2338
QY 1680 CTCCAGACGACCAACAAGATATGACAGGAGATCATTTCCAGGAATTTATGATGCTGT 1739

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DB 2339 CTCACAGCAGCCACACAGTATGACGGGAGTCATCCAGAAATTTATGATGCTCTGT 2398
OY 1740 TTGATATTGAAGCAAGTGGACCTTCCAAAGGCGTGGGAGATGTAAGACAGATTT 1799
DB 2399 TTGATATTGAAGCAAGTGGACCTTCCAAAGGCGTGGGAGATGTAAGACAGATTT 2458
OY 1800 CTGTTCAGGCTTCACAGTGCAGGACCTGCAGAGACTTTGATGAGTAAAGG 1859
DB 2459 ATGTTCAGGCTTCACAGTGCAGGACCTGCAGAGACTTTGATGAGTAAAGG 2518
OY 1860 ATTCTTTAGAGACTCTGATATTGATTTGTGTGATGTCCTC--AAAGATATATG 1917
DB 2519 ATTCTTTAGAGAAATCCGATATTGATTTGTGTGATGTCCTCAGAAAGATGTAATGC 2578
OY 1918 GTATATGATATAATTTAAATTTGATATTGTAATTAATATATATATAA 1977
DB 2579 GTATATGATATAATTTAAATTTGATATTGTAATTAATATATATATAA 2638
OY 1978 AAAAAAAAAAAAAA 1992
DB 2639 AAAAAAAAAAAAAA 2653

RESULT 6
ABL69670
ID ABL69670 standard; DNA: 2653 BP.
XX
AC ABL69670:
XX
DT 15-MAY-2002 (first entry)
XX
DE Prostate cancer related gene sequence SEQ ID NO:8007.
XX
KM Human: cancer: colon; breast; ovary; oesophagus; kidney; thyroid;
KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KM cytoskeletal; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KM gene; ds.
XX
OS Homo sapiens.
XX
PN M0200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001MO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-208531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234505P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
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PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI: 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 8007; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytoskeletal
CC activity and can be used, in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;

Query Match 85.5%; Score 1702.6; DB 24; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

OY 240 AGGTTAAATGCCCAGCTGGCAGGGGCCAAAGAGTCATCTCTACTGAGCCCTGCG 299
DB 899 AGGTTAAATGCCCAGCTGGCAGGGGCCAAAGAGTCATCTCTACTGAGCCCTGCG 958
OY 300 ACTACTTGGCTGCTGGGGTGAAGTCCATATCCAGAGCGTGGATCTTCGAGGTG 359
DB 959 ACTACTTGGCTGCTGGGGTGAAGTCCATATCCAGAGCGTGGATCTTCGAGGTG 1018
OY 360 TCCAGCGTGAATATCTGAATCTGAATGCTGACAGACCTCTCACACAGGTTACC 419
DB 1019 TCCAGCGTGAATATCTGAATCTGAATGCTGACAGACCTCTCACACAGGTTACC 1078
OY 420 CAGCAATGATACGCTTATAGCATGGAATTGACAGAGCTGTGCTCCCAAGATTTC 479
DB 1079 CAGCAATGATATGCTTATAGCGTGAATTCAGAGGCTGTGCTCCCAAGATTTC 1138
OY 480 CTGTTCACTCAGTTGATCTATGATGCACAGAGCTCTAGAAAAAATGGTGGCTCAG 539
DB 1139 CTGTTCACTCAGTTGATCTATGATGCACAGAGCTCTAGAAAAAATGGTGGCTCAG 1198
```

QY 540 CACCACAGATAGCAGCTGGAGAGAAAGTCTCAAAAGTCCATATGTTGACCGGCT 599
 |||||
 Db 1199 CACACACAGATAGCAGCTGGAGAGAAAGTCTCAAAAGTCCATATGTTGACCGGCT 1258
 QY 600 TTACTGGAAACCTTTCTACACAAAAGTCAAGATGCATCCACTCTACCAATGAAGTGA 659
 |||||
 Db 1259 TTACTGGAAACCTTTCTACACAAAAGTCAAGATGCATCCACTCTACCAATGAAGTGA 1318
 QY 660 CGGAATTTACATGTGATAGTACTCTAGAGAGACAGTGAACAGACAGATATGTCA 719
 |||||
 Db 1319 CAGGAATTTACATGTGATAGTACTCTAGAGAGACAGTGAACAGACAGATATGTCA 1378
 QY 720 TTCTGGAGAGTCAACCGGAGCTCATGGGTGTTGGTATTTGACCCCTCAGAGTGAAGCAG 779
 |||||
 Db 1379 TTCTGGAGAGTCAACCGGAGCTCATGGGTGTTGGTATTTGACCCCTCAGAGTGAAGCAG 1438
 QY 780 CTGTGTTTCATGAACTGTGAGAGAGCTTTTGGAACTGAAGAAAGAGGGTGAAGCTTA 839
 |||||
 Db 1439 CTGTGTTTCATGAAATGTGAGAGAGCTTTGGAACCTGAAGAAAGAGGGTGAAGCTTA 1498
 QY 840 GAAGAACAAATTTGTTGCAAGCTGGGATGCAAGAAATTTGGTCTTCTGGTCTACAG 899
 |||||
 Db 1499 GAAGAACAAATTTGTTGCAAGCTGGGATGCAAGAAATTTGGTCTTCTGGTCTACAG 1558
 QY 900 AGTGGCGAGAGATTAATTAAGACTCTTCAAGAGCGTGGCGCTTAATTAATGCTG 959
 |||||
 Db 1559 AGTGGCGAGAGATTAATTAAGACTCTTCAAGAGCGTGGCGCTTAATTAATGCTG 1618
 QY 960 ACTCATCTATAGAGAGAACTACACTCTGAGAGTGTATGTACACCACTGATGTACAGCT 1019
 |||||
 Db 1619 ACTCATCTATAGAGAGAACTACACTCTGAGAGTGTATGTACACCACTGATGTACAGCT 1678
 QY 1020 TGGTATACCAACCTAAACAAAGAGCTGAAGCCCTATGAGGCTTTGAAGGAAATCTC 1079
 |||||
 Db 1679 TGGTATACCAACCTAAACAAAGAGCTGAAGCCCTATGAGGCTTTGAAGGAAATCTC 1738
 QY 1080 TTTATGAAAGTGGACTAAAAAGTCTTCCCAAGTTCAGTGGCATGCCAGAGATTA 1139
 |||||
 Db 1739 TTTATGAAAGTGGACTAAAAAGTCTTCCCAAGTTCAGTGGCATGCCAGAGATTA 1798
 QY 1140 GCAAAATTTGGAGTCTGAAAAATGATTTTGAAGTGTCTTCCACAGCACTTGAATTTGCTCAG 1199
 |||||
 Db 1799 GCAAAATTTGGAGTCTGAAAAATGATTTTGAAGTGTCTTCCACAGCACTTGAATTTGCTCAG 1858
 QY 1200 GGAGAGCAGGATTAATAAATTTGGGAAACAAACAAATTCACGGGCTATCCACTGTATC 1259
 |||||
 Db 1859 GGAGAGCAGGATTAATAAATTTGGGAAACAAACAAATTCACGGGCTATCCACTGTATC 1918
 QY 1260 ACAGTGTCTATGAACATATGAGTGTGGAAAAAGTTTTATGATTCCAATGTTTAAATATTC 1319
 |||||
 Db 1919 ACAGTGTCTATGAACATATGAGTGTGGAAAAAGTTTTATGATTCCAATGTTTAAATATTC 1978
 QY 1320 ACCTCACTGTGGCCCGAGTTCGAGAGGAGTGTGTTGAGCTAGCCAAATTCATAGTGC 1379
 |||||
 Db 1979 ACCTCACTGTGGCCCGAGTTCGAGAGGAGTGTGTTGAGCTAGCCAAATTCATAGTGC 2038
 QY 1380 TCCCTTTGATGTGAGATTAATGCTGTGTTTGAAGAAATGCTGTGACAAATCTTACA 1439
 |||||
 Db 2039 TCCCTTTGATGTGAGATTAATGCTGTGTTTGAAGAAATGCTGTGACAAATCTTACA 2098
 QY 1440 AATATTTCTATGAACATCCACAGAAATGAGACATACAGTATATGATTTGATTCCTTT 1499
 |||||
 Db 2099 GATATTTCTATGAACATCCACAGAAATGAGACATACAGTATATGATTTGATTCCTTT 2158
 QY 1500 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAAAGTTCAGCGAGAGACTCCAGACT 1559
 |||||
 Db 2159 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAAAGTTCAGCGAGAGACTCCAGACT 2218
 QY 1560 TTGACAAAAGCAACCAATATTTGTAAGATGATGATGATCAACCTGATTTCTTGGA 1619
 |||||
 Db 2219 TTGACAAAAGCAACCAATATTTGTAAGATGATGATGATCAACCTGATTTCTTGGA 2278

QY 1620 GAGCATTTATGATCCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATG 1679
 |||||
 Db 2279 GAGCATTTATGATCCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATG 2338
 QY 1680 CTCGAAGCAGCCACAACAAGTATGAGGGGAGTCAATCCAGGAATTTATGATGCTGCT 1739
 |||||
 Db 2339 CTCGAAGCAGCCACAACAAGTATGAGGGGAGTCAATCCAGGAATTTATGATGCTGCT 2398
 QY 1740 TTGATATTGAAGCAAGTGGAGCCCTTCCAAAGGCTGGGGAGATGTGAAGACACATTT 1799
 |||||
 Db 2399 TTGATATTGAAGCAAGTGGAGCCCTTCCAAAGGCTGGGGAGATGTGAAGACACATTT 2458
 QY 1800 CTGTTCAGCCTTTCACAGTGCAGAGAGCTGCAGAGACTTTGAGTGAAGTAAAGCAGAG 1859
 |||||
 Db 2459 AGTTCAGCCTTTCACAGTGCAGAGAGCTGCAGAGACTTTGAGTGAAGTAAAGCAGAG 2518
 QY 1860 ATTCTTTAGAGACTCTGATATGAAATTTGTGTGATGTCATCTC --AAAGAAATTAATG 1917
 |||||
 Db 2519 ATTCTTTAGAGACTCTGATATGAAATTTGTGTGATGTCATCTCAGAAAGAAATCGTAATG 2578
 QY 1918 GTATATTGAATTAATTTTAAATTTGATATTTGAATTAAGTGAATTTATATATATA 1977
 |||||
 Db 2579 GTATATTGAATTAATTTTAAATTTGATATTTGAATTAAGTGAATTTATATATATA 2638
 QY 1978 AAAAAAAAAAAAAA 1992
 |||||
 Db 2639 AAAAAAAAAAAAAA 2653

RESULT 7
 AB083845
 ID AB083845 standard; cdna; 2653 bp.
 XX
 AC AB083845;
 XX
 DT 03-FEB-2003 (first entry)
 XX
 DE Human P5MA encoding cDNA SEQ ID NO:7.
 DE
 KW Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 KW T cell; enzyme; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200281646-A2.
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002MO-US11101.
 PF
 PR 06-APR-2001; 2001US-282211P.
 PR 07-NOV-2001; 2001US-337017P.
 PR 07-MAR-2002; 2002US-363210P.
 XX
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.
 PI
 PI Simard JTL, Diamond DC, Liu L, Xie Z;
 XX
 DR WPI; 2003-067518/06.
 DR
 DR P-PSDB; ABP74131.
 XX
 PT Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 PT encoding the peptides, that are useful epitopes of target-associated
 PT antigens -
 PS
 PS Claim 1; Page 149-151; 352pp; English.
 XX
 CC The present invention describes an isolated epitope (I) and an epitope
 CC cluster. Also described is a vaccine or immunotherapeutic composition
 CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
 CC creating an animal, by administering to an animal the vaccine or
 CC immunotherapeutic composition. VC is also useful for evaluating
 CC immunogenicity of a vaccine or immunotherapeutic composition, by

Db	2463	GAGCATTATTGATCCATTTAGGGTTACACAGACGCCCTTTTATAGGCATGTACTATG	2522
QY	1680	CTCCAGACGACCACACAGATATGCAGGGGAGTCATTCCAGAAATTATGATGCTGT	1739
Db	2523	CTCCAGAGCGCACACAGATATGCAGGGGAGTCATTCCAGAAATTATGATGCTGT	2582
QY	1740	TTGATATTGAAGCAAAAGTGGACCCCTTCCAAAGCGCTGGGAGATGTGAAGAGACAGATT	1799
Db	2383	TTTGATATTGAAGCAAAAGTGGACCCCTTCCAAAGCGCTGGGAGATGTGAAGAGACAGATT	2642
QY	1800	CTGTGCGACGCTTACAGTGCAGCGACCTGCAGAGACTTTCAGTGAAGTAAAGCTCAAGAG	1859
Db	2643	ATGTTGACGCTTACAGTGCAGCGACCTGCAGAGACTTTCAGTGAAGTAAAGCTCAAGAG	2702
QY	1860	ATTCTTTTAGACACTCTGTATTGAATTGTGTGTATGTCACTC--AAAGATAATAATGG	1917
Db	2703	ATTCTTTTAGAAMAACCGTATTGAATTGTGTGTATGTCACTCAGAAAGAACTCAATAG	2762
QY	1918	GTAATATTGATTAATTTTAAATTTGCTAATTTTGAATTAAGATTAATTAATTAATTA	1977
Db	2763	GTAATATTGATTAATTTTAAATTTGCTAATTTTGAATTAAGATTAATTAATTAATTA	2822
QY	1978	AAAAAAAAAAAAAAAA 1992	
Db	2823	AAAAAAAAAAAAAAAA 2837	

RESULT 9	
ABV23013	
ID	ABV23013 standard; cDNA; 2884 BP.
XX	
AC	ABV23013;
XX	
DT	13-SEP-2002 (first entry)
XX	
DE	Human prostate expression marker cDNA 23004.
XX	
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW	pharmacogenomic marker; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200160860-A2.
XX	
PD	23-AUG-2001.
XX	
PE	20-FEB-2001; 2001WO-US05171.
XX	
PR	17-FEB-2000; 2000US-183319P.
PR	16-MAR-2000; 2000US-189862P.
PR	25-MAY-2000; 2000US-207454P.
PR	09-JUN-2000; 2000US-211314P.
PR	18-JUL-2000; 2000US-219007P.
PR	13-DEC-2000; 2000US-255281P.
XX	
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
PI	Schlegel R, Endege WO, Monahan JE;
XX	
DR	WPI; 2001-662795/76.
XX	
PT	Novel isolated nucleic acid molecule associated with cancerous state of
XX	prostate cells and correlating with presence of prostate cancer, useful
PT	for detecting presence of prostate cancer; Stage of prostate cancer -
XX	
PS	Claim 1; Page 4097-4098; 11750pp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule (I) comprising
CC	a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC	specification or its complement. (I) is useful for:
CC	(a) assessing whether a patient is afflicted with prostate cancer;
CC	(b) monitoring the progression of prostate cancer in a patient;
CC	

CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other;
SQ

Query Match	85.5%	Score 1702.6	DB 23	Length 2884	
Best Local Similarity	98.5%	Pred. No. 0			
Matches 1729	Conservative	0	Mismatches 24	Indels 2	Gaps 1
QY	240	AGGTTAAAAAGCCAGCTGGCAGGGGCCAAGAGAGTCATCTTCTACTCAGACCCGTGCTG	239		
DB	1083	AGGTTAAAAATGCGCCAGCTGGCAGGGGCCAAGAGAGTCATCTTCTACTCCGACCCCTGCTG	1142		
QY	300	ACTACTTTCCTCCTGGGGTGAAGTCCTATCCAGACGGTGGAAATCTTCGGAGGGGTG	359		
DB	1143	ACTACTTTCCTCCTGGGGTGAAGTCCTATCCAGATGGTGGAAATCTTCGGAGGGGTG	1202		
QY	360	TCCAGCGTGAAGAAATCCTTAATCTGATGGTGCAGAGAGACCCCTCCACACAGTTACC	419		
DB	1203	TCCAGCGTGAAGAAATCCTTAATCTGATGGTGCAGAGAGACCCCTCCACACAGTTACC	1262		
QY	420	CAGCAAAATGAATACGCTTATATAGCATGGAAATTCGACAGGCTGTGGTCTTCCAAAGTATC	479		
DB	1263	CAGCAAAATGAATACGCTTATATAGCGGTGAATATGAGAGCGTGGTCTTCCAAAGTATC	1322		
QY	480	CTGTTTCATCCAGTTGGATACATATCATGACACAGAGCTCCCTAGAAAAATGGGTGGCTCAG	539		
DB	1323	CTGTTTCATCCATTTGGATACATATCATGTATGACACGAAGCTCCCTAGAAAAATGGGTGGCTCAG	1382		
QY	540	CACCACAGATAGCAGCTGGAGAGAGACTCAAAATGTCTCTACATGTTGGACCTGGCT	599		
DB	1383	CACCACCGATAGCAGCTGGAGAGAGACTCAAAAGTCCCTACAAATGGTGACCTGGCT	1442		
QY	600	TTACTCGAAACCTTTCTACAAAAAGCAGAGATGACATCCATCTACCAATCAAGTGA	659		
DB	1443	TTACTCGAAACCTTTCTACAAAAAGTCAAGATGACATCCATCTACCAATCAAGTGA	1502		
QY	660	CGAGAAATTTACAAATGTGATAGTACTCTCAAGAGAGCAGTGGAAACGACAGATATGTCA	719		
DB	1503	CGAGAAATTTACAAATGTGATAGTACTCTCAAGAGAGCAGTGGAAACGACAGATATGTCA	1562		
QY	720	TTCTGGGAGGTCACCGGACATCANTGGGTGTTGGTGGTATTGACCCTCAGAGTGGACAG	779		
DB	1563	TTCTGGGAGGTCACCGGACATCANTGGGTGTTGGTGGTATTGACCCTCAGAGTGGACAG	1622		
QY	780	CTGTTGTTTCATGAAACCTGTGAGAGAGCTTTGGAACACTGAAAAAGAGGGTGGAGACTTA	839		
DB	1623	CTGTTGTTTCATGAAATTTGTGAGAGACTTTGGAACTGAAAAAGAGGGTGGAGACTTA	1682		
QY	840	GAGAACAATTTTGTTCAGAGCTGGGATGCAGAGAAATTTGGTCTCTTGCTTCTACTG	899		
DB	1683	GAGAACAATTTTGTTCAGAGCTGGGATGCAGAGAAATTTGGTCTCTTGCTTCTACTG	1742		
QY	900	AGTGGGACAGAGATTAATCAAGACTCCCTCAAGAGCGGGGTGGCTTATATTAATCTG	959		
DB	1743	AGTGGGACAGAGATTAATCAAGACTCCCTCAAGAGCGGGGTGGCTTATATTAATCTG	1802		
QY	960	ACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTTGTACACCACTGATGTACAGT	1019		
DB	1803	ACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTTGTACACCCGTGATGTACAGT	1862		
QY	1020	TGCTATACACCTTAACAAAAGAGCTGAAAACCCCTGATGAAAGGCTTTGAAGCAAAATCTC	1079		
DB	1863	TGCTATACACCTTAACAAAAGAGCTGAAAACCCCTGATGAAAGGCTTTGAAGCAAAATCTC	1922		


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QY 1080 TTTATGAAAGTGGACTATAAAAAAGTCTTCCOCAGAGTTCAGTGGCATGCCAGATAA 1139
DB 1923 TTTATGAAAGTGGACTATAAAAAAGTCTTCCOCAGAGTTCAGTGGCATGCCAGATAA 1982
QY 1140 GCAAAATGGGATCTGGAATGATTTTGAAGTGTCTTCCAGAGACTTGAATTGTCTGAG 1199
DB 1983 GCAAAATGGGATCTGGAATGATTTTGAAGTGTCTTCCAGAGACTTGAATTGTCTGAG 2042
QY 1200 GGAGAGCAGGTATCTATAAAATTTGGGAAACAACAATTCAGCGGCTATCCAGCTATC 1259
DB 2043 GGAGAGCAGGTATCTATAAAATTTGGGAAACAACAATTCAGCGGCTATCCAGCTATC 2102
QY 1260 ACAGTCTATGAAACATATGAGTGTGGTGAAGTATTTATGATCCAAATGTTAAATATC 1319
DB 2103 ACAGTCTATGAAACATATGAGTGTGGTGAAGTATTTATGATCCAAATGTTAAATATC 2162
QY 1320 ACCCTACGTGGCCAGGTTCCAGAGAGGATGTGTTTGAAGTACCAATTCATATGTC 1379
DB 2163 ACCCTACGTGGCCAGGTTCCAGAGAGGATGTGTTTGAAGTACCAATTCATATGTC 2222
QY 1380 TCCCTTTGATGTGGAGATTATGCTGATGTTTAAAGAAATGCTGCAAAATCTACA 1439
DB 2223 TCCCTTTGATGTGGAGATTATGCTGATGTTTAAAGAAATGCTGCAAAATCTACA 2282
QY 1440 ATATTTCTATGAACATCCACAGAAATGAAACATACAGTTATCATTTGATTCCTT 1499
DB 2283 GATTTTCTATGAACATCCACAGAAATGAAACATACAGTTATCATTTGATTCCTT 2342
QY 1500 TTTTTCAGTATAAAATTTTACAGAAATGCTTCCAGTTCACGAGAGATCCAGACT 1559
DB 2343 TTTTTCAGTATAAAATTTTACAGAAATGCTTCCAGTTCACGAGAGATCCAGACT 2402
QY 1560 TTGACAAAAGCAACCATTTGTTAAGAAATGATGATGATCAACTCATTTTGGGAA 1619
DB 2403 TTGACAAAAGCAACCATTTGTTAAGAAATGATGATGATCAACTCATTTTGGGAA 2462
QY 1620 GAGCATTTATGATCATTAGGTTACACAGAGACCTTTTATAGCATGTCTATG 1679
DB 2463 GAGCATTTATGATCATTAGGTTACACAGAGACCTTTTATAGCATGTCTATG 2522
QY 1680 CTCGCAAGCGCCACAACAGTATGCAAGGGAGTCAATCCAGAAATTTGATGCTCT 1739
DB 2523 CTCGCAAGCGCCACAACAGTATGCAAGGGAGTCAATCCAGAAATTTGATGCTCT 2582
QY 1740 TTGATTTGAAAGCAAGTGAGACCTTCCAGGCGTGGGAGATGGAAGAGACAGATT 1799
DB 2583 TTGATTTGAAAGCAAGTGAGACCTTCCAGGCGTGGGAGATGGAAGAGACAGATT 2642
QY 1800 CTGTTGACGCTTCAAGTGCAGGAGCTGCAGAGACTTGAAGTGAAGTACCTTAAGAG 1859
DB 2643 ATGTTGACGCTTCAAGTGCAGGAGCTGCAGAGACTTGAAGTGAAGTACCTTAAGAG 2702
QY 1860 ATTTCTTAGAGACTGTGATTTGAATTTGTGTGATGTCTACTC--AAACAATTAATATG 1917
DB 2703 ATTTCTTAGAGACTGTGATTTGAATTTGTGTGATGTCTACTC--AAACAATTAATATG 2762
QY 1918 GATATTTGATTAATTTTAAATTTGATATTTGAATTAAGTTGAATTTATATATATAA 1977
DB 2763 GATATTTGATTAATTTTAAATTTGATATTTGAATTAAGTTGAATTTATATATATAA 2822
QY 1978 AAAAAAAAAAAAAA 1992
DB 2823 AAAAAAAAAAAAAA 2837

RESULT 10
ID ABV28703 standard: cDNA: 2884 BP.
XX ABV28703:
AC
XX
XX 16-SEP-2002 (first entry)
XX
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DE Human prostate expression marker cDNA 28694.
XX
XX Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene: SS.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PE 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 6024-6025; 11750bp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other;
XX
Query Match 85.5%; Score 1702.6; DB 23; Length 2884;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
QY 240 AGTTAAATAATGCCAGCTGCGAGAGGGCCCAAGGAGTCAATCTACTACAGACCTGCTG 299
DB 1083 AGTTAAATAATGCCAGCTGCGAGAGGGCCCAAGGAGTCAATCTACTACAGACCTGCTG 1142
QY 300 ACTACTTCTCTCTGGGGTGAAGTCTTATCCAGAGAGGTTGGAATCTTCTGAGAGTGTG 359
DB 1143 ACTACTTCTCTCTGGGGTGAAGTCTTATCCAGATGCTTCTCTGAGAGTGTG 1202
QY 360 TCCAGCGTGAATATCTTAATCTGAATGAGGAGGAGACCTCTCACACAGGTTACC 419
DB 1203 TCCAGCGTGAATATCTTAATCTGAATGAGGAGGAGACCTCTCACACAGGTTACC 1262
QY 420 CAGCAATGAATAGCTTATAGCATGGAATTCAGAGGCTGTGCTTCCAAATATTC 479
DB 1263 CAGCAATGAATAGCTTATAGCATGGAATTCAGAGGCTGTGCTTCCAAATATTC 1322
QY 480 CTGTTTCATCCAGTGTGATCTATGATGCGACAGAACTCTTAAATAAAAGGGTGGCTGAG 539
DB 1323 CTGTTTCATCCAGTGTGATCTATGATGCGACAGAACTCTTAAATAAAAGGGTGGCTGAG 1382
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OY 540 CACCACCAGATAGCAGCTGAGAGAGAGTCTCAAGTGTCTCAATGTTGACCTGGCT 599
    |||||||
Db 1383 CACCACCAGATAGCAGCTGAGAGAGAGTCTCAAGTGTCTCAATGTTGACCTGGCT 1442
OY 600 TTACTGGAACCTTTCTACACAAAAGTCAAGATGCATCTCACTACCAATGAAGTGA 659
    |||||||
Db 1443 TTACTGGAACCTTTCTACACAAAAGTCAAGATGCATCTCACTACCAATGAAGTGA 1502
OY 660 CGAAGATTTCAAATGTGATAGTACTCTCAGAGAGCAGTGAACACAGACAGATATGTCA 719
    |||||||
Db 1503 CAGAAGTTTCAATGTGATAGTACTCTCAGAGAGCAGTGAACACAGACAGATATGTCA 1562
OY 720 TTCTGGAGGTCAACCGGACTCATGGGTGTTGGTGTATTTGACCCCTCAAGATGGAGAG 779
    |||||||
Db 1563 TTCTGGAGGTCAACCGGACTCATGGGTGTTGGTGTATTTGACCCCTCAAGATGGAGAG 1622
OY 780 CTGTGTTCATGAACCTGAGAGGCTTTGGAACACTGAAAAGAGAGGGTGGAGACCTA 839
    |||||||
Db 1623 CTGTGTTCATGAACCTGAGAGGCTTTGGAACACTGAAAAGAGAGGGTGGAGACCTA 1682
OY 840 GAAGAACAAATTTGTTTGCAGCTGGAGTCCAGAAATTTGCTCTTCTTGTTCTACTG 899
    |||||||
Db 1683 GAAGAACAAATTTGTTTGCAGCTGGAGTCCAGAAATTTGCTCTTCTTGTTCTACTG 1742
OY 900 AGTGGCAGAGAGATATTCAGACTCCTTCAGAGCTGGCGTGGCTTATTTATATCTG 959
    |||||||
Db 1743 AGTGGCAGAGAGATATTCAGACTCCTTCAGAGCTGGCGTGGCTTATTTATATCTG 1802
OY 960 ACCTATCTATAGAGAACTACACTCTGAGAGTGTATTTGACACCACTGATGACAGCT 1019
    |||||||
Db 1803 ACCTATCTATAGAGAACTACACTCTGAGAGTGTATTTGACACCACTGATGACAGCT 1862
OY 1020 TGGTATCAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAGAGCTTTGAAGCAATCTC 1079
    |||||||
Db 1863 TGGTATCAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAGAGCTTTGAAGCAATCTC 1922
OY 1080 TTTATGAAAGTTGGACTTAACAAAAGTCCCTCCAGAGTTGAGTGCATGCCCCAGATTA 1139
    |||||||
Db 1923 TTTATGAAAGTTGGACTTAACAAAAGTCCCTCCAGAGTTGAGTGCATGCCCCAGATTA 1982
OY 1140 GCAATTTGGAGTCTGAGAAATGATTTGGTGTCTTCCAGAGCTTGGATTTCTCTCAG 1199
    |||||||
Db 1983 GCAATTTGGAGTCTGAGAAATGATTTGGTGTCTTCCAGAGCTTGGATTTCTCTCAG 2042
OY 1200 GCAGAGCAGCGTATACATAAAATTTGGAAACAAACAATTCAGCGGCTATCCACTGTATC 1259
    |||||||
Db 2043 GCAGAGCAGCGTATACATAAAATTTGGAAACAAACAATTCAGCGGCTATCCACTGTATC 2102
OY 1260 ACAGTGTCTATGAACATATGATGTTGGTGAAGAAAGTTTATGATCCAAATGTTTAAATATC 1319
    |||||||
Db 2103 ACAGTGTCTATGAACATATGATGTTGGTGAAGAAAGTTTATGATCCAAATGTTTAAATATC 2162
OY 1320 ACCTCAGTGTGGCCAGGTTGAGAGAGGATGTTGTTGAGCTGAGCCATTCATAGTGC 1379
    |||||||
Db 2163 ACCTCAGTGTGGCCAGGTTGAGAGAGGATGTTGTTGAGCTGAGCCATTCATAGTGC 2222
OY 1380 TCCCTTTTGATTCGAGATTAATGCTGTAGTTTAAAGAAATATGCTGACAAAATCTACA 1439
    |||||||
Db 2223 TCCCTTTTGATTCGAGATTAATGCTGTAGTTTAAAGAAATATGCTGACAAAATCTACA 2282
OY 1440 ATATTTCTATGAACATCCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTT 1499
    |||||||
Db 2283 GTATTTCTATGAACATCCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTT 2342
OY 1500 TTCTGCGATGAAGAAATTTTACAGAAATGCTTCCCAATTCAGAGAGAGCTCCAGAGCT 1559
    |||||||
Db 2343 TTCTGCGATGAAGAAATTTTACAGAAATGCTTCCCAATTCAGAGAGAGCTCCAGAGCT 2402
OY 1560 TTGACAAAAGCACCACATATTTGTAAGATGATGAATGATCAACTGTTTCTGAGAA 1619
    |||||||
Db 2403 TTGACAAAAGCACCACATATTTGTAAGATGATGAATGATCAACTGTTTCTGAGAA 2462
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OY 1620 GAGCATTTATTTGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATCTATG 1679
    |||||||
Db 2463 GAGCATTTATTTGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATCTATG 2522
OY 1680 CTCCAAGCAGCCCAACAAGTATGACAGGAGTCAATCCAGAAATTTATGATGCTCTGT 1739
    |||||||
Db 2523 CTCCAAGCAGCCCAACAAGTATGACAGGAGTCAATCCAGAAATTTATGATGCTCTGT 2582
OY 1740 TTATTTTGAAGCAAGTGGAGCCCTTCCAGAGCCTGGGAGATGTAAGAGACAGATTT 1799
    |||||||
Db 2583 TTGATTTTGAAGCAAGTGGAGCCCTTCCAGAGCCTGGGAGATGTAAGAGACAGATTT 2642
OY 1800 CTGTTCAGCCTTCACAGTGCAGAGCTGACAGAGCTTTGATGTAAGTACCTTAAGAG 1859
    |||||||
Db 2643 ATGTTCAGCCTTCACAGTGCAGAGCTGACAGAGCTTTGATGTAAGTACCTTAAGAG 2702
OY 1860 ATCTTTAGAGACTCTGTATTTGAATTTGTGTGTATGCTACTC - AAAGATATATATG 1917
    |||||||
Db 2703 ATCTTTAGAGAAATCCGTATTTGATTTGTGTGTATGCTACTCAGAAAGATGTAATG 2762
OY 1918 GTATATGATTAATTTTAAATTTGATATTTGAATTAAGTGAATATATATATATAA 1977
    |||||||
Db 2763 GTATATGATTAATTTTAAATTTGATATTTGAATTAAGTGAATATATATATATAA 2822
OY 1978 AAAAAAAAAAAAAA 1992
    |||||||
Db 2823 AAAAAAAAAAAAAA 2837

RESULT 11
ABY28849
ID ABY28849 standard; cDNA; 2884 BP.
XX
AC ABY28849;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 28840.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189863P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI: 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
prostate cells and correlating with presence of prostate cancer, useful
for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1: Page 6076-6077; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
```

CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other;

Query Match 85.5%; Score 1702.6; DB 23; Length 2884;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 240 AGGTTAAATGCCCCAGCTGGAGGGCCAAAGAGTCTTCTACTAGACCCCTCTG 289
 DB 1083 AGGTTAAATGCCCCAGCTGGAGGGCCAAAGAGTCTTCTACTAGACCCCTCTG 1142
 QY 300 ACTACTTTGCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCTGAGGTG 359
 DB 1143 ACTACTTTGCTCTGGGGTGAAGTCTATCCAGATGGTGAATCTTCTGAGGTG 1202
 QY 360 TCCAGCGTGAATATCTTAATCTGAATGTGAGAGACCCCTCCAGCCAGTTAC 419
 DB 1203 TCCAGCGTGAATATCTTAATCTGAATGTGAGAGACCCCTCCAGCCAGTTAC 1262
 QY 420 CAGCAATGATAGCTTATAGGATGGAATTCAGAGGCTGTGTCTTCCAGTATTC 479
 DB 1263 CAGCAATGATAGCTTATAGGATGGAATTCAGAGGCTGTGTCTTCCAGTATTC 1322
 QY 480 CTGTTCATCAGTGTGATATGATGACAGAGACTCCCTAGAAAAAATGGTGGCTAG 539
 DB 1323 CTGTTCATCAGTGTGATATGATGACAGAGACTCCCTAGAAAAAATGGTGGCTAG 1382
 QY 540 CACACACAGATAGCTGAGAGAGAAAGTCAAAAGTCTCAATGTGGACCTGGCT 599
 DB 1383 CACACACAGATAGCTGAGAGAGAAAGTCTCAAAAGTCTCAATGTGGACCTGGCT 1442
 QY 600 TTACTGAAACTTTTCTACACAAAAAGTCAAGATGCATCCACTTACCAATGAAATGA 659
 DB 1443 TTACTGAAACTTTTCTACACAAAAAGTCAAGATGCATCCACTTACCAATGAAATGA 1502
 QY 660 CGAGATTTTCAATGTGATGATCTCTCAGAGAGCAGTGAACACAGAGATATGTCA 719
 DB 1503 CGAGATTTTCAATGTGATGATCTCTCAGAGAGCAGTGAACACAGAGATATGTCA 1562
 QY 720 TTCTGGAGGTCAACGGGACTCATGGGTGTTGGTGTATTAACCCCTCAAGTGGAGCAG 779
 DB 1563 TTCTGGAGGTCAACGGGACTCATGGGTGTTGGTGTATTAACCCCTCAAGTGGAGCAG 1622
 QY 780 CTGTGTTCATGAACTGTGAGAGCTTTTGAACACTGAAAGAAAGGTTGAGACTTA 839
 DB 1623 CTGTGTTCATGAACTGTGAGAGCTTTTGAACACTGAAAGAAAGGTTGAGACTTA 1682
 QY 840 GAAGAACAAATTTTGTTCAGAGCTGGATGCAGAGAAATTTGCTTGTGTTTACTG 899
 DB 1683 GAAGAACAAATTTTGTTCAGAGCTGGATGCAGAGAAATTTGCTTGTGTTTACTG 1742
 QY 900 AGTGGGAGAGATTAATCAAGACTCCTTCAAGAGGCTGGGCTTATTAATAGCTG 959
 DB 1743 AGTGGGAGAGATTAATCAAGACTCCTTCAAGAGGCTGGGCTTATTAATAGCTG 1802
 QY 960 ACTCATCTATAGAGAACTTACACTCTGAGAGTTGATTTTACACACTGATGTACAGCT 1019
 DB 1803 ACTCATCTATAGAGAACTTACACTCTGAGAGTTGATTTTACACACTGATGTACAGCT 1862
 QY 1020 TGGTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAGCAAAATCTC 1079
 DB 1863 TGGTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAGCAAAATCTC 1922

QY 1080 TTTATGAAGTGGAGTAAAGAAAGTCCCTCCAGAGTTCAGTGCATGCCAGATTA 1139
 DB 1923 TTTATGAAGTGGAGTAAAGAAAGTCCCTCCAGAGTTCAGTGCATGCCAGATTA 1982
 QY 1140 GCAAAATGGGATCGGAAATGATTTGAGGTGTTCTTCCAGAGTTCGAAATGCTTCAG 1199
 DB 1983 GCAAAATGGGATCGGAAATGATTTGAGGTGTTCTTCCAGAGTTCGAAATGCTTCAG 2042
 QY 1200 GCAGAGCAGGATTAATAAATTTGGGAAACAAATTCACGGCTATCCACTGATC 1259
 DB 2043 GCAGAGCAGGATTAATAAATTTGGGAAACAAATTCACGGCTATCCACTGATC 2102
 QY 1260 ACAGTGTCTATGAACATATGAGTGTGGAAGAAATTTATGATCCAAATTTAAATATC 1319
 DB 2103 ACAGTGTCTATGAACATATGAGTGTGGAAGAAATTTATGATCCAAATTTAAATATC 2162
 QY 1320 ACCCTACGTGAGCCAGGTTCCAGAGAGATGAGTGTGAGCTAGCCAAATTCATAGTGC 1379
 DB 2163 ACCCTACGTGAGCCAGGTTCCAGAGAGATGAGTGTGAGCTAGCCAAATTCATAGTGC 2222
 QY 1380 TCCCTTTGATTTGTGAGATTAATGCTGTAGTTTAAAGAAATGCTGACAAATCTACA 1439
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 QY 1440 ATATTTCTATGAACATCCACAGGAAATGAAGACATCACTTATATCATTTGATCACTT 1499
 DB 2283 ATATTTCTATGAACATCCACAGGAAATGAAGACATCACTTATATCACTTATTTGATTCACCTTT 2342
 QY 1500 TTTCTGAGTAAATAATTTTACAGAAATTCCTTCCAGATTCAGAGAGACTCCAGACT 1559
 DB 2343 TTTCTGAGTAAATAATTTTACAGAAATTCCTTCCAGATTCAGAGAGACTCCAGACT 2402
 QY 1560 TTGCAAAACCAACCAATTTTGTGAAGATGATGAATGATCAATCTATCTTTCTGAAA 1619
 DB 2403 TTGCAAAACCAACCAATTTGATGAATGATGAATGATCAATCTATCTTTCTGAAA 2462
 QY 1620 GAGCATTTATGATCCATTTAGGTTTACACAGAGACTTTTATAGGATGATCATATG 1679
 DB 2463 GAGCATTTATGATCCATTTAGGTTTACACAGAGACTTTTATAGGATGATCATATG 2522
 QY 1680 CTCCAAGCAGCCCAACCAATGATGAGGAGTCAATCCAGAAATTTATGATGCTCTGT 1739
 DB 2523 CTCCAAGCAGCCCAACCAATGATGAGGAGTCAATCCAGAAATTTATGATGCTCTGT 2582
 QY 1740 TTGATATTTGAAGCAAGTGGACCTTCCAGAGCTTGGGAGATGTGAAGACAGATTT 1799
 DB 2583 TTGATATTTGAAGCAAGTGGACCTTCCAGAGCTTGGGAGATGTGAAGACAGATTT 2642
 QY 1800 CTGTGAGGCTTCCAGAGTGCAGGAGCTGCAGAGACTTTGAGTGAAGTGGCTAAGAG 1859
 DB 2643 ATGTGAGGCTTCCAGAGTGCAGGAGCTGCAGAGACTTTGAGTGAAGTGGCTAAGAG 2702
 QY 1860 ATTCTTTAGAGCTCTGATTTGAATTTGCTGTATGTCACTC - AAAGAAATATATG 1917
 DB 2703 ATTCTTTAGAGCTCTGATTTGAATTTGCTGTATGTCACTCAGAAAGATGATATG 2762
 QY 1918 GTATATTTGAATTTTAAATTTGATATTTGAATTAAGGTTGATATATATATAA 1977
 DB 2763 GTATATTTGAATTTTAAATTTGATATTTGAATTAAGGTTGATATATATATAA 2822
 QY 1978 AAAAAAAAAAAAAA 1992
 DB 2823 AAAAAAAAAAAAAA 2837

RESULT 12
 AAT36785
 ID AAT36785 standard; cdna; 2654 BP.
 AC AAT36785;
 XX
 DT 04-NOV-1996 (first entry)

XX	Prostate-specific membrane antigen CDNA.
XX	Prostate-specific membrane antigen; PSM; promoter; prostate cancer;
KM	metastasis; gene therapy; diagnosis; ss.
OS	Homo sapiens.
XX	
XX	Key
FT	Location/Qualifiers
FT	5'UTR
FT	1..261
FT	/*tag= a
FT	262..2253
FT	/*tag= b
FT	/product= PSM antigen
FT	misc.feature
FT	114..380
FT	/*tag= C
FT	/note= "bases 114-380 (-147 to +109) are absent
FT	In PSM' CDNA"
FT	polya_signal
FT	2352..2357
FT	/*tag= d
XX	
XX	W09626272-A1.
XX	
XX	29-AUG-1996.
XX	
XX	23-FEB-1996; 96WO-US02424.
XX	
XX	02-JUN-1995; 95US-0470735.
XX	24-FEB-1995; 95US-0394152.
XX	02-JUN-1995; 95US-0466381.
XX	
XX	(SLOK) SLOAN KETTERING INST CANCER RES.
XX	
XX	Fair WR, Heston MDW, Israeli RS;
XX	
XX	WPI: 1996-402365/40.
XX	P-PSDB: AAW02234.
XX	
XX	DNA encoding alternatively spliced prostate-specific membrane
XX	antigen - useful to develop prods. for detecting haematogenous
XX	micrometastatic tumour cells; or prostate cancer progression
XX	
XX	Example 1; Fig 47A-D; 284pp; English.
XX	
XX	A CDNA clone (AA136785) codes for human 100 kDa prostate-specific
XX	membrane (PSM) antigen (AAW02234), an integral membrane glycoprotein
XX	that is very highly expressed in prostatic tumours and metastases.
XX	CC It was obtd. from lymph node carcinoma of prostate (LNCAP) cell
XX	mRNA by PCR amplification (see also AA136795-808) and screening of an
XX	LNCAP CDNA library using an amplified cDNA partial clone as probe.
XX	CC The CDNA can be used to provide probes and primers useful e.g. in
XX	detecting hematogenous micrometastatic tumour cells and determining
XX	prostate cancer progression (see also AA136827-30 and AA136813-18),
XX	and in gene therapy. An alternatively spliced PSM, PSM', has a
XX	shorter CDNA sequence. PSM genomic DNA is given in AA136786.
XX	
XX	Sequence 2654 BP; 782 A; 525 C; 639 G; 708 T; 0 other;
XX	
XX	Query Match 84.8%; Score 1690; DB 17; Length 2654;
XX	Best Local Similarity 98.4%; Pred. No. 0;
XX	Matches 1728; Conservative 0; Mismatches 25; Indels 3; Gaps 2;
XX	
XX	240 AGCTTAAATGCGCCAGCTGGCAGGGGCCAAGAGCATCTCTACTACAGACCTGGTG 299
XX	
XX	899 AGGTTAAATGCGCCAGCTGGCAGGGGCCAAGAGCATCTCTACTACAGACCTGGTG 958
XX	
XX	300 ACTATTGCTCTGCGGTGGAAGTCTTACAGAGCGTTGGAATCTTCTGAGAGTGCTG 359
XX	
XX	959 ACTATTGCTCTGCGGTGGAAGTCTTACAGAGCGTTGGAATCTTCTGAGAGTGCTG 1018
XX	
XX	360 TCCACGCTGGAATATCTCTAAATCTGAATGCTGACAGAGACCTCTACACAGGTATCC 419
XX	
XX	1019 TCCACGCTGGAATATCTCTAAATCTGAATGCTGACAGAGACCTCTACACAGGTATCC 1078
XX	

QY	420	CAGCAAAATGAAATACGCTTTATAGCGATGGAATTGCAGAGCGCTGTGGTCTTCCAAATATTC	479
Db	1079	CAGCAAAATGAAATATGCTTTATAGCGGTGGAATTTGCAGAGCGCTGTGGTCTTCCAAATATTC	1138
QY	480	CTGTTTCATCCAGTGTGATCTATGATGATCCACAGAAAGCTCCAGAAAAAATGGGGTGCACG	539
Db	1139	CTGTTTCATCCAGTGTGATCTATGATGATCCACAGAAAGCTCCAGAAAAAATGGGGTGCACG	1198
QY	540	CACCACCAAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCTCAATGTTTGACCTGGCT	599
Db	1199	CACCACCAAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCTCAATGTTTGACCTGGCT	1258
QY	600	TTACTGGAAACTTTCTTCACAAAAAAGTCCAAAGATCCACCTCTACCAATGAAGTCA	659
Db	1259	TTACTGGAAACTTTCTTCACAAAAAAGTCCAAAGATCCACCTCTACCAATGAAGTCA	1318
QY	660	CGAGAAATTTACATGTATAGTATAGTCTCCAGAGAGCAGTGGACCAAGACAGATATGTCA	719
Db	1319	CGAGAAATTTACATGTATAGTATAGTCTCCAGAGAGCAGTGGACCAAGACAGATATGTCA	1378
QY	720	TTCTGGGAGGTCCACCGGACTCATNGGTTGTTGGTATTTGACCTCCAGAGTGGACG	779
Db	1379	TTCTGGGAGGTCCACCGGACTCATNGGTTGTTGGTATTTGACCTCCAGAGTGGACG	1438
QY	780	CTGTTGTTTCATGAAGACCTGTGAGAGCTTTGGAACTCGAAAAAGGAAGGTGTGAGACCTA	839
Db	1439	CTGTTGTTTCATGAAGACCTGTGAGAGCTTTGGAACTCGAAAAAGGAAGGTGTGAGACCTA	1498
QY	840	GAAGAAACAATTTGTTTGGCAAGCTGGGATGCAGAGAATTTGGTCTTCTTGTTCTACAG	899
Db	1499	GAAGAAACAATTTGTTTGGCAAGCTGGGATGCAGAGAATTTGGTCTTCTTGTTCTACAG	1558
QY	900	AGTGGGCGAGAGATATATTCAGACTCCCTCAAGAGCGTGGCGGCTTATATTAATGCTG	959
Db	1559	AGTGGGCGAGAGATATATTCAGACTCCCTCAAGAGCGTGGCGGCTTATATTAATGCTG	1618
QY	960	ACTCATCTATGGAAGAACTACACTCTGAGAGTTGATTTTACACCACTGATGTACAGCT	1019
Db	1619	ACTCATCTATGGAAGAACTACACTCTGAGAGTTGATTTTACACCACTGATGTACAGCT	1678
QY	1020	TGCTATACACCTAACAAAGAGCTGAAAAGCCCTGATGAAAGCTTTGAAGGGAAATCTC	1079
Db	1679	TGCTATACACCTAACAAAGAGCTGAAAAGCCCTGATGAAAGCTTTGAAGGGAAATCTC	1738
QY	1080	TTTATGAAAGTTGACATCTAAAAAAGTCCCTCCAGAGTTCCAGTGGCATCCCGAGATAA	1139
Db	1739	TTTATGAAAGTTGACATCTAAAAAAGTCCCTCCAGAGTTCCAGTGGCATCCCGAGATAA	1798
QY	1140	GCAAAATTTGGGATCTGGAAATGATTTTGAAGTGTCTTCCAAAGCACTTGGAAATGCTCAG	1199
Db	1799	GCAAAATTTGGGATCTGGAAATGATTTTGAAGTGTCTTCCAAAGCACTTGGAAATGCTCAG	1858
QY	1200	GCAGAGCACGAGTATCTAAAAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC	1259
Db	1859	GCAGAGCACGAGTATCTAAAAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC	1918
QY	1260	ACAGTGTCTATGAAAACATATGAGTGTGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1919	ACAGTGTCTATGAAAACATATGAGTGTGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1978
QY	1320	ACCTACAGTGGCCGAGGTGCGAGAGGAGGATGAGTGTGACCTAGCCAAATCCATAGTGC	1379
Db	1979	ACCTACAGTGGCCGAGGTGCGAGAGGAGGATGAGTGTGACCTAGCCAAATCCATAGTGC	2038
QY	1380	TCCCTTTGATTTGTGAGATTAATGCTGTAGTTTTAAGAAAGTATGTCACAAAATCTACA	1439
Db	2039	TCCCTTTGATTTGTGAGATTAATGCTGTAGTTTTAAGAAAGTATGTCACAAAATCTACA	2098
QY	1440	ATATTTCTATGAAAACATCCACAGGAAATGAAAGACATACAGTTTATTCATTTGATTCACCTT	1499
Db	2099	ATATTTCTATGAAAACATCCACAGGAAATGAAAGACATACAGTTTATTCATTTGATTCACCTT	2158

XX
PA (GETH) GENENTECH INC.

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

DR WPI; 2001-602746/68.
DR P-PSDB; AAU29075.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and PT to screen for modulators of the compounds -

PS Claim 2; Fig 103; 774pp; English.

Sequence 2558 BP; 745 A; 509 C; 623 G; 681 T; 0 other;

50 Sequence 2558 BP; 745 A; 509 C; 623 G; 681 T; 0 other;

Query Match	84.7%;	Score 1687.2;	DB 22;	Length 2558;
Best Local Similarity	98.6%;	Pred. No. 0;		

Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY	240	AGGTTAAAAATGCCACAGTGGCAGGAGGGCCAAAGAGATCTTCTACTCAGACCCCTGCTG	299
Db	821	AGGTTAAAAAATGCCACAGTGGCAGGAGGGCCAAAGAGATCTTCTACTCAGACCCCTGCTG	880
QY	300	ACTACTTTCGCCCTGGGGGTGAAGTCCATCCAGACAGGTGTGAATCTTCTGGAGGTGGTG	359
Db	881	ACTACTTTCGCCCTGGGGGTGAAGTCCATCCAGACAGGTGTGAATCTTCTGGAGGTGGTG	940
QY	360	TTCAGCGTGGAAATATCTCTAAATCTGAATGCTGCAGAGAGACCTCTCAGACCGAGTTTACC	419
Db	941	TTCAGCGTGGAAATATCTCTAAATCTGAATGCTGCAGAGAGACCTCTCAGACCGAGTTTACC	1000
QY	420	CAGCAAAATGAATAGCGCTTATAGCATGGAAATTCAGAGAGCGCTGTGGCTTCCAGATATTC	479
Db	1001	CAGCAAAATGAATAGCGCTTATAGCATGGAAATTCAGAGAGCGCTGTGGCTTCCAGATATTC	1060
QY	480	CTGTTCATCCAGTTGGATCTATGATGCACAGAAAGCTCTAGAAAAATGGGTGGCTCAG	539
Db	1061	CTGTTCATCCAGTTGGATCTATGATGCACAGAAAGCTCTAGAAAAATGGGTGGCTCAG	1120
QY	540	CACACACAGATAGCAGCTGGAGAGAGAGTCCAAAGTGCCTCAATAGTTGGACCTGGCT	599
Db	1121	CACACACAGATAGCAGCTGGAGAGAGAGTCCAAAGTGCCTCAATAGTTGGACCTGGCT	1180
QY	600	TTACTGGAACCTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA	659
Db	1181	TTACTGGAACCTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA	1240
QY	660	CGAACAATTTCAATGTGATAGTGCCTCCAGAGAGAGCAGTGGAAACCGAGACGATATATGCA	719
Db	1241	CGAACAATTTCAATGTGATAGTGCCTCCAGAGAGAGCAGTGGAAACCGAGACGATATATGCA	1300
QY	720	TTCTGGAGAGTCAACGGGACTCATGGGTGTTTGGTGTATTGACCTCAGAGTGGAGCAG	779
Db	1301	TTCTGGAGAGTCAACGGGACTCATGGGTGTTTGGTGTATTGACCTCAGAGTGGAGCAG	1360

QY	780	TTGTTGTTCAAGAAACGTGTGAGAGCTTTGGACAACATGAAAACGAAGCGTGGAGACTA	839
Db	1361	CTGTTGTTCAAGAAATGTGTGAGAGCTTTGGACAACGTGAAAAGAGGGGTGGAGACTA	1420
QY	840	GAAGAACAAATTTTGTTCGAAGCTGGGGTGCAGAGAATTTGGTCTCTTGTGTTCTACTG	899
Db	1421	GAAGAACAAATTTGTTCGAAGCTGGGGTGCAGAGAATTTGGTCTCTTGTGTTCTACTG	1480
QY	900	AGTGGCAGAGGATTAATTCAGAGCTCCTTCAGAGCGTGGCGTGGCTTAATTAATGCTG	959
Db	1481	AGTGGCGAGAGAAATTCAGAGCTCCTTCAGAGCGTGGCGTGGCTTAATTAATGCTG	1540
QY	960	ACATCATCTATGAAGGAACATACACTCTGAGAGTGGATTGTAACACCACTGATGTACAGCT	1019
Db	1541	ACTCATCTATGAAGGAACATACACTCTGAGAGTGGATTGTAACACCGCTGATGTACAGCT	1600
QY	1020	TGTTATACACCTTAACAAAAGAGCTGAAAAGCCCTGATGAAGCGCTTTGAAGGCAAAATCTC	1079
Db	1601	TGTTATACACCACTTAACAAAAGAGCTGAAAAGCCCTGATGAAGCGCTTTGAAGGCAAAATCTC	1660
QY	1080	TTTATGAAAGCTTGGACATTAATAAAGTCTCTCCCAAGTTCAGTGGCATGCCCCAGATTA	1139
Db	1661	TTTATGAAAGCTTGGACATTAATAAAGTCTCTCCCAAGTTCAGTGGCATGCCCCAGATTA	1720
QY	1140	GCAAAATGGGATCTGGAAATGATTTTGAAGTGTCTTCCAAAGCATGGATTTGGAATTCCTTCAG	1199
Db	1721	GCAAAATGGGATCTGGAAATGATTTTGAAGTGTCTTCCAAAGCATGGATTTGGAATTCCTTCAG	1780
QY	1200	GCAGAGCAGCGTATACTTAATAATGGGAACAACAATTCAGCGGCTATTCACACTGTATC	1259
Db	1781	GCAGAGCAGCGTATACTTAATAATGGGAACAACAATTCAGCGGCTATTCACACTGTATC	1840
QY	1260	ACAGTGTCTATGAAGCAATATGATGTGGGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1841	ACAAGTGTCTATGAAGCAATATGATGTGGGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1900
QY	1320	ACCTCACGTGTGCCAGGTTTCGAGAGAGGATGTTGAGCTAGCCAAATTCATAGTGC	1379
Db	1901	ACCTCACGTGTGCCAGGTTTCGAGAGAGGATGTTGAGCTAGCCAAATTCATAGTGC	1960
QY	1380	TTCCTTTTGAATGTGCGAGATTAATCTGTAGTTTTAAAGATATGCGACAAAATCTACA	1439
Db	1961	TTCCTTTTGAATGTGCGAGATTAATCTGTAGTTTTAAAGATATGCGACAAAATCTACA	2020
QY	1440	ATATTTTATGAAGCAATCCACAGGAATGAAGACATACAGTTTATCATTTGATTCACATTT	1499
Db	2021	GTATTTTATGAAGCAATCCACAGGAATGAAGACATACAGTTTATCATTTGATTCACATTT	2080
QY	1500	TTTCTGCAAGTAAAAATTTTACAGAAATTTGTTCCAAAGTTTACGCGACAGACTCCAGACT	1559
Db	2081	TTTCTGCAAGTAAAAATTTTACAGAAATTTGTTCCAAAGTTTACGCGACACTCCAGACT	2140
QY	1560	TTGCAAAAAGCAACCCCAATATTTGTTAAGATGATGAATGATCACTGATGTTCTGGAAA	1619
Db	2141	TTGCAAAAAGCAACCCCAATATTTAAGAAATGATGAATGATCACTGATGTTCTGGAAA	2200
QY	1620	GAGCATTTATGATCATTTAGGGTTTACACAGACAGACTTTTATATAGGCATGTCACTATG	1679
Db	2201	GAGCATTTATGATCATTTAGGGTTTACACAGACAGACTTTTATATAGGCATGTCACTATG	2260
QY	1680	CTCCAGCAGCCACAACAAGTATCCAGGGGAGTCATCCAGAAATTTATATAGTCTCTGT	1739
Db	2261	CTCCAGCAGCCACAACAAGTATCCAGGGGAGTCATCCAGAAATTTATATAGTCTCTGT	2320
QY	1740	TTGATATTTGAAGCAAGTGGACCTTCCAAAGGCGTGGGGAGATGTAAGAGACAGATTT	1799
Db	2321	TTGATATTTGAAGCAAGTGGACCTTCCAAAGGCGTGGGGAGATGTAAGAGACAGATTT	2380
QY	1800	CTGTTTGCAGCCTTACACAGTGCAGGCAGCTGCAGAGACTTTGATGAAGATGACCTAAGAG	1859
Db	2381	ATGTTTGCAGCCTTACACAGTGCAGGCAGCTGCAGAGACTTTGATGAAGATGACCTAAGAG	2440

PR	11-JUN-1998;	9805-088863P.
PR	11-JUN-1998;	9805-088876P.
PR	12-JUN-1998;	9805-089090P.
PR	12-JUN-1998;	9805-089105P.
PR	16-JUN-1998;	9805-089512P.
PR	16-JUN-1998;	9805-089514P.
PR	17-JUN-1998;	9805-089538P.
PR	17-JUN-1998;	9805-089538P.
PR	17-JUN-1998;	9805-089538P.
PR	18-JUN-1998;	9805-089538P.
PR	19-JUN-1998;	9805-089532P.
PR	22-JUN-1998;	9805-090246P.
PR	22-JUN-1998;	9805-090252P.
PR	22-JUN-1998;	9805-090254P.
PR	24-JUN-1998;	9805-090429P.
PR	24-JUN-1998;	9805-090435P.
PR	24-JUN-1998;	9805-090444P.
PR	24-JUN-1998;	9805-090461P.
PR	24-JUN-1998;	9805-090535P.
PR	24-JUN-1998;	9805-090540P.
PR	25-JUN-1998;	9805-090676P.
PR	25-JUN-1998;	9805-090678P.
PR	25-JUN-1998;	9805-090688P.
PR	25-JUN-1998;	9805-090690P.
PR	25-JUN-1998;	9805-090694P.
PR	25-JUN-1998;	9805-090695P.
PR	25-JUN-1998;	9805-090696P.
PR	26-JUN-1998;	9805-090862P.
PR	26-JUN-1998;	9805-090863P.
PR	26-JUN-1998;	9805-091010P.
PR	01-JUL-1998;	9805-091359P.
PR	01-JUL-1998;	9805-091544P.
PR	02-JUL-1998;	9805-091478P.
PR	02-JUL-1998;	9805-091486P.
PR	02-JUL-1998;	9805-091626P.
PR	02-JUL-1998;	9805-091628P.
PR	02-JUL-1998;	9805-091632P.
PR	04-JUL-1998;	9805-094006P.
PR	04-AUG-1998;	9805-095282P.
PR	10-AUG-1998;	9805-095988P.
PR	10-AUG-1998;	9805-096012P.
PR	17-AUG-1998;	9805-096757P.
PR	17-AUG-1998;	9805-096766P.
PR	17-AUG-1998;	9805-096867P.
PR	17-AUG-1998;	9805-096891P.
PR	17-AUG-1998;	9805-096897P.
PR	18-AUG-1998;	9805-096949P.
PR	18-AUG-1998;	9805-096959P.
PR	18-AUG-1998;	9805-097022P.
PR	26-AUG-1998;	9805-097952P.
PR	26-AUG-1998;	9805-097954P.
PR	26-AUG-1998;	9805-097955P.
PR	26-AUG-1998;	9805-097971P.
PR	26-AUG-1998;	9805-097974P.
PR	26-AUG-1998;	9805-098014P.
PR	01-SEP-1998;	9805-098716P.
PR	01-SEP-1998;	9805-098723P.
PR	02-SEP-1998;	9805-098803P.
PR	02-SEP-1998;	9805-098821P.
PR	02-SEP-1998;	9805-098843P.
PR	09-SEP-1998;	9805-099602P.
PR	10-SEP-1998;	9805-099741P.
PR	10-SEP-1998;	9805-099754P.
PR	10-SEP-1998;	9805-099763P.
PR	10-SEP-1998;	9805-099812P.

Query Match 84.7%; Score 1687.2; DB 25; Length 2558;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 240 AGGTTAAATGCCCCAGCTGGCAGGCGCCAAAGAGTCAATCTCTCTAGACCCCTGCTG 299
 Db 821 AGGTTAAATGCCCCAGCTGGCAGGCGCCAAAGAGTCAATCTCTCTAGACCCCTGCTG 880


Qy	300	ACTACTTGTCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCTGGAGGTGTC 359
Db	881	ACTACTTGTCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCTGGAGGTGTC 940
Qy	360	TCCAGCGTGAATATCTTAATCTGAATGTGTGACAGACCCCTCTCACACGAGTTACC 419
Db	941	TCCAGCGTGAATATCTTAATCTGAATGTGTGACAGACCCCTCTCACACGAGTTACC 1000
Qy	420	CAGCAATGAATATGCTTATAGCATGAATTCAGAGCTGTGGTCTTCCAGATATTC 479
Db	1001	CAGCAATGAATATGCTTATAGCGTGAATTCAGAGCTGTGGTCTTCCAGATATTC 1060
Qy	480	CTGTTCATCAGTTGATATCTATGATGACAGAGCTCTTAGAAAAATGGGTGCTCAG 539
Db	1061	CTGTTCATCAGTTGATATCTATGATGACAGAGCTCTTAGAAAAATGGGTGCTCAG 1120
Qy	540	CACACACAGATAGCAGCTGGAGAGAGTCTCAAGTGTCTTCAATGTTGGACCTGCT 599
Db	1121	CACACACAGATAGCAGCTGGAGAGAGTCTCAAGTGTCTTCAATGTTGGACCTGCT 1180
Qy	600	TTACTGGAACCTTTTCTACACAAAAAGTCAAGTGCATCTCACTTACCAATGAAGTGA 659
Db	1181	TTACTGGAACCTTTTCTACACAAAAAGTCAAGTGCATCTCACTTACCAATGAAGTGA 1240
Qy	660	CGAGATTTTACATGTGATAGTACTCTCAGAGGACAGTGGAAACAGACAGATATGTCA 719
Db	1241	CGAGATTTTACATGTGATAGTACTCTCAGAGGACAGTGGAAACAGACAGATATGTCA 1300
Qy	720	TTCTGGAGGTACCCGGGCTCATGGGTGTTGGTGTATGACCTTCAGAGTGAAGCAG 779
Db	1301	TTCTGGAGGTACCCGGGCTCATGGGTGTTGGTGTATGACCTTCAGAGTGAAGCAG 1360
Qy	780	CTGTGTTTATGAACTGTGAGAGCTTTGGAACCTGAAAAAGAGGCTGGAGACCTTA 839
Db	1361	CTGTGTTTATGAACTGTGAGAGCTTTGGAACCTGAAAAAGAGGCTGGAGACCTTA 1420
Qy	840	GAAAGCAATTTTGTGGAAGTGGATGACAAATTTGGTCTTGGTTCAGTAC 899
Db	1421	GAAAGCAATTTTGTGGAAGTGGATGACAAATTTGGTCTTGGTTCAGTAC 1480
Qy	900	AGTGGCAGAGATAATTAAGACTCTTCAAGAGCGTGGCTTATATTAATGCTG 959
Db	1481	AGTGGCAGAGATAATTAAGACTCTTCAAGAGCGTGGCTTATATTAATGCTG 1540
Qy	960	ACTCATCTATAGAGAACTACACTGTAGAGTTATTTGTACACAGATGTACAGCT 1019
Db	1541	ACTCATCTATAGAGAACTACACTGTAGAGTTATTTGTACACAGATGTACAGCT 1600
Qy	1020	TGCTATACCACTTAACAAAGAGCTGAAAAAGCTGATGAAGCTTTGAAGCAATCTC 1079
Db	1601	TGCTATACCACTTAACAAAGAGCTGAAAAAGCTGATGAAGCTTTGAAGCAATCTC 1660
Qy	1080	TTTATGAAGTTGGACTAATAAAAGTCTTCCCAAGTTCAGTGGCATGCCAGATTA 1139
Db	1661	TTTATGAAGTTGGACTAATAAAAGTCTTCCCAAGTTCAGTGGCATGCCAGATTA 1720
Qy	1140	GCAATTTGGATCTGAAATGATTTGAGGTGTTCTTCCAGAGCTTGAATTCGTTGAG 1199
Db	1721	GCAATTTGGATCTGAAATGATTTGAGGTGTTCTTCCAGAGCTTGAATTCGTTGAG 1780
Qy	1200	GCAGAGCAGGTATATTAATAAATTTGGAAACAAATTCAGCGGCTTTCACCTATTC 1259
Db	1781	GCAGAGCAGGTATATTAATAAATTTGGAAACAAATTCAGCGGCTTTCACCTATTC 1840
Qy	1260	ACAGTGTATGAACATATGAGTTGGTGAAGATTTTATGATCCAAATGTTAAATATC 1319
Db	1841	ACAGTGTATGAACATATGAGTTGGTGAAGATTTTATGATCCAAATGTTAAATATC 1900
Qy	1320	ACCTGCTGTGGCCCGGTTTCGAGAGGAGATGTTTATAGCTAGCCAAATTCATATGTC 1379
Db	1901	ACCTGCTGTGGCCCGGTTTCGAGAGGAGATGTTTATAGCTAGCCAAATTCATATGTC 1960

OY 1380 TCCCTTTGATGTGAGATTATGCTGTAGTTTAAAGATATGCTGACAAAACTACA 1439
|||||
Db 1961 TCCCTTTGATGTGAGATTATGCTGTAGTTTAAAGATATGCTGACAAAACTACA 2020
|||||
OY 1440 ATATTCTATGAACATCCACAGGAATGAGACATACATTTATCATTTGATCAGCTT 1439
|||||
Db 2021 GTATTCTATGAACATCCACAGGAATGAGACATACATTTATCATTTGATCAGCTT 2080
|||||
OY 1500 TTTCTGCAGTAAAAATTTTACAGAAATGCTCCAAAGTTCAGCAGAGACTCCAGACT 1559
|||||
Db 2081 TTTCTGCAGTAAAAATTTTACAGAAATGCTCCAAAGTTCAGCAGAGACTCCAGACT 2140
|||||
OY 1560 TTGACAAAAGCAACCCAAATTTGTTAAGATGATGATGATCACTATGTTCTGAAA 1619
|||||
Db 2141 TTGACAAAAGCAACCCAAATTTGTTAAGATGATGATGATCACTATGTTCTGAAA 2200
|||||
OY 1620 GAGCATTTATGATCCATTAGGTTACACAGACCTTTTATAGCATGTCATCTATG 1679
|||||
Db 2201 GAGCATTTATGATCCATTAGGTTACACAGACCTTTTATAGCATGTCATCTATG 2260
|||||
OY 1680 CTCCAAGCAGCCACAACTATGACAGGAGATCATTTCCAGAAATTTATGATGCTCTGT 1739
|||||
Db 2261 CTCCAAGCAGCCACAACTATGACAGGAGATCATTTCCAGAAATTTATGATGCTCTGT 2320
|||||
OY 1740 TTGATATTGAAGCAAAAGTGAACCTTCCAAAGCCCTGGGAGATGTGAAGACAGATTT 1799
|||||
Db 2321 TTGATATTGAAGCAAAAGTGAACCTTCCAAAGCCCTGGGAGATGTGAAGACAGATTT 2380
|||||
OY 1800 CTGTTGCAGCCTTCACAGTGCAGGACGCTGACAGACTTTGAGTAAGTACCTTAAGAG 1859
|||||
Db 2381 AAGTTGCAGCCTTCACAGTGCAGGACGCTGACAGACTTTGAGTAAGTACCTTAAGAG 2440
|||||
OY 1860 ATTCTTTAGACTCTGTATTTGAATTTGTTGTGTATGTCACTC--AAAGATAATTAATGG 1917
|||||
Db 2441 ATTTTGTAGAGATCCGTAATTTGTGTGTATGTCACTCAGAAAGAAATCGTAATGG 2500
|||||
OY 1918 GTATATTGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATATTTATATATA 1975
|||||
Db 2501 GTATATTGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATATTTATATATA 2558
|||||

Search completed: October 4, 2003, 16:52:20
Job time : 664 secs

RT "Molecular characterization of human brain N-acetylated alpha-linked
RT acidic dipeptidase (NAA1Ldase).";
RL J. Pharmacol. Exp. Ther. 286:1020-1025(1998).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM PSMA-1), AND CHARACTERIZATION.
RC TISSUE-Prostate;
RX MEDLINE-99185063; PubMed-10085079;
RA Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,
RA van der Helm L., Fraiponts E., Ashton D., Gordon R.D.;
RA "Isolation and expression of novel human glutamate carboxypeptidases
RT with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
RT peptidase IV activity.";
RL J. Biol. Chem. 274:8470-8483(1999).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS PSMA-1 AND PSMA-2), AND VARIANT HHC
RP TYR-475.
RC TISSUE-Jejunum;
RX MEDLINE-20545101; PubMed-11092159;
RA Devlin A.M., Ling E.-H., Pearson J.M., Fernando S., Clarke R.,
RA Smith A.D., Halsted C.H.;
RA "Glutamate carboxypeptidase II: a polymorphism associated with lower
RT levels of serum folate and hyperhomocysteinemia.";
RL Hum. Mol. Genet. 9:2837-2844(2000).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM PSMA-5).
RA Peace D.J., Zhang Y., Holt G., Ferrer K.T., Heller M., Sosman J.A.,
RA Xue B.H.;
RT "Identification of three novel splice variants of prostate-specific
RT membrane antigen.";
RN Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
RP [9]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS PSMA-3 AND PSMA-4).
RA Lupold S.E., Ciley S.C., Coffey D.S.;
RL "Alternative Splicing of the prostate-specific membrane antigen.";
RN Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
RP [10]
RP SEQUENCE OF 60-74, AND SUBCELLULAR LOCATION.
RC TISSUE-Prostatic carcinoma;
RX MEDLINE-99025849; PubMed-9809977;
RA Grauer L.S., Lawler K.D., Marignac J.L., Kumar A., Goel A.S.,
RA Wolfert R.L.;
RT "Identification, purification, and subcellular localization of
RT prostate-specific membrane antigen PSM' protein in the LNCaP prostatic
RL carcinoma cell line";
RN Cancer Res. 58:4787-4789(1998).
RL [11]
RP ALTERNATIVE SPLICING.
RA Bodega T., She D., Turi T., Wroblewska B., Neale J.H.;
RT "Molecular cloning of alternatively spliced variants of the peptidase
RT against N-acetylaspartylglutamate (NAAG) from human and rat nervous
RT systems.";
RL Abstr. - Soc. Neurosci. 24:579-579(1998).
RN [12]
RP CHARACTERIZATION.
RX MEDLINE-98288196; PubMed-9622670;
RA Luthi-Carter R., Barczak A.K., Speno H.D., Coyle J.T.;
RT "Hydrolysis of the neuropeptide N-acetylaspartylglutamate (NAAG) by
RL cloned human glutamate carboxypeptidase II.";
RN Brain Res. 795:341-348(1998).
RN [13]
RP DOMAIN STRUCTURE.
RX MEDLINE-97330810; PubMed-9187245;
RA Rawlings N.D., Barrett A.J.;
RT "Structure of membrane glutamate carboxypeptidase.";
RN Biochim. Biophys. Acta 1339:247-252(1997).
RN [14]
RP MOTAGENESIS.
RX MEDLINE-99102317; PubMed-9882712;
RA Speno H.S., Luthi-Carter R., Macias W.L., Valentine S.L.,
RA Joshi A.R.T., Coyle J.T.;
RT "Site-directed mutagenesis of predicted active site residues in
RL glutamate carboxypeptidase II.";
RN Mol. Pharmacol. 55:179-185(1999).

CC -1- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-
CC acidic dipeptidase (NALADase) activity. Has a preference for tri-
CC alpha-glutamate peptides. In the intestine, required for the
CC uptake of folate. In the brain, modulates excitatory
CC neurotransmission through the hydrolysis of the neuropeptide, N-
CC acetylaspartylglutamate (NAAG), thereby releasing glutamate. Stable
CC at pH greater than 6.5. Isoforms PSN-4 and PSN-5 would appear to
CC be physiologically irrelevant. Involved in prostate tumor
CC progression.
CC
CC -1- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity.
CC
CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl gamma.
CC -1- COFACTOR: Zinc; Binds two ions per subunit. Required for NALADase
CC activity.
CC
CC -1- ENZYME REGULATION: The NALADase activity is inhibited by beta-
CC NAAG, quisqualic acid, 2-(phosphonomethyl) pentanedioic acid
CC (EMPA) and EDTA. Activated by cobalt.
CC
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane.
CC The PSMA isoform is cytoplasmic.
CC
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=6;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=PSMA-1;
CC IsoId=Q04609-1; Sequence=Displayed;
CC Name=PSMA-2;
CC IsoId=Q04609-2; Sequence=VSP_005341;
CC Name=PSMA-3;
CC IsoId=Q04609-3; Sequence=VSP_005342;
CC Name=PSMA-4;
CC IsoId=Q04609-4; Sequence=VSP_005339, VSP_005340;
CC Name=PSMA-5;
CC IsoId=Q04609-5; Sequence=VSP_005337, VSP_005338;
CC Name=PSMA'
CC
CC IsoId=Q04609-6; Sequence=VSP_005336;
CC
CC -1- TISSUE SPECIFICITY: Highly expressed in prostate epithelium. Also
CC expressed, in the small intestine, brain, kidney, liver, spleen,
CC colon and the capillary endothelium of a variety of tumors.
CC Expressed specifically in jejunum brush border membranes. In the
CC brain, highly expressed in the ventral striatum and brain stem. In
CC the prostate, the PSMA' cytosolic isoform is the most abundant
CC form in normal tissue, the membrane-bound PSMA-1 form in primary
CC prostate tumors. The PSMA-2 isoform also found in normal prostate
CC as well as in brain and liver.
CC
CC -1- INDUCTION: In the prostate, up-regulated in response to androgen
CC deprivation.
CC
CC -1- DOMAIN: The NALADase activity is found in the central region, the
CC dipeptidyl peptidase IV type activity in the C-terminal.
CC
CC -1- PM: The first two amino acids at the N-terminus of isoform PSMA'
CC appear to be cleaved by limited proteolysis.
CC
CC -1- PM: The N-terminus is blocked.
CC
CC -1- DISEASE: Defects in FOLH1 may be a cause of hyperhomocysteinemia
CC (HHC), a condition associated with increased risk of
CC cardiovascular disease, neural tube defects, and cognitive
CC deficits.
CC
CC -1- MISCELLANEOUS: PSMA is used as a diagnostic and prognostic
CC indicator of prostate cancer, and as a possible marker for various
CC neurological disorders such as schizophrenia, Alzheimer's disease
CC and Huntington's disease.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC -----
OR EMBL; M99487; AAA60209.1; -
OR EMBL; S76978; AAB3750.2; -
OR EMBL; AF007544; AAC83972.1; -

Query Match 98.2% Score 2288; DB 1; Length 750; 

Best Local Similarity 98.0%; Pred. No. 2.7e-16;

Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY	1	MGGSAPPDSSWRGSLKYSYVNGPFGTGNFTQYKMHHSHTNEYRIYVIGTLGAVER	60
Db	309	MGGSAPPDSSWRGSLKYPVNYGPGFTGNFTQYKMHHSHTNEYRIYVIGTLGAVER	368
QY	61	DRYVILGHRDSSWFGGIDPOSGAAVYHEIYRSFGTLAKBGMRRPRTILFASMDAEEFGL	120
Db	369	DRYVILGHRDSSWFGGIDPOSGAAVYHEIYRSFGTLAKBGMRRPRTILFASMDAEEFGL	428
QY	121	LGSTEMADNSRLLOEGVAYINADSSIEGVYTLRVDCPTPLMYSLVNLTLELSPDEGF	180
Db	429	LGSTEMADNSRLLOEGVAYINADSSIEGVYTLRVDCPTPLMYSLVNLTLELSPDEGF	488
QY	181	EGKSLYESWTKKSPSPFSGMPRIKSLGSGNDFEVEFQRLGIASGRARYTKNWTNKFSG	240
Db	489	EGKSLYESWTKKSPSPFSGMPRIKSLGSGNDFEVEFQRLGIASGRARYTKNWTNKFSG	548
QY	241	YPLHSHYETVELYERKYDDPEKHLHYAQRGMVFELANSIYLPECCRDYAVYLKRYA	300
Db	549	YPLHSHYETVELYERKYDDPEKHLHYAQRGMVFELANSIYLPECCRDYAVYLKRYA	608
QY	301	DKIYINSMKRPQEKKTYSLSFDSLFSAVKNPTEIASKSEKSEKLOPDKSNPILIRKMNOL	360
Db	609	DKIYINSMKRPQEKKTYSLSFDSLFSAVKNPTEIASKSEKSEKLOPDKSNPILIRKMNOL	668
QY	361	MLETARAFIDPLGLDRPFYRHVIYAPSSHNKYAGESEFGIYDALFDEISKVDPKRWGDY	420
Db	669	MLETARAFIDPLGLDRPFYRHVIYAPSSHNKYAGESEFGIYDALFDEISKVDPKRWGEV	728
QY	421	KROIYVAFTVQAAAEFTLSEYA 442	
Db	729	KROIYVAFTVQAAAEFTLSEYA 750	

RESULT 2

FOHL_PIG STANDARD; PRT; 751 AA.

AC 077564;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate carboxypeptidase) (MGCC) (N-acetylated alpha-linked acidic dipeptidase 1) (NALADase 1) (Pteroylpolyp-gamma-glutamate carboxypeptidase) (Folypolypoly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase 1) (Prostate-specific membrane antigen homolog).

GN FOHL1 OR NALAD1.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OC NCB1;taxid=9823;

OX

RN

RP

RC

RC TISSUE=Jejunal mucosa;

RC MEDLINE=98352082; PubMed=968595;

RA Halsted C.H., Ling E.-H., Luthi-Carter R., Villanueva J.A., Gardner J.M., Coyle J.T.;

RA Halsted C.H., Ling E.-H., Luthi-Carter R., Villanueva J.A., Gardner J.M., Coyle J.T.;

RT "Folypolypoly-gamma-glutamate carboxypeptidase from pig jejunum. Molecular characterization and relation to glutamate carboxypeptidase II.";

RT J. Biol. Chem. 273:20417-20424(1998).

RL

RN

[2]

RP

RP ERRATUM.

RA Halsted C.H., Ling E.-H., Luthi-Carter R., Villanueva J.A., Gardner J.M., Coyle J.T.;

RA J. Biol. Chem. 275:30746-30746(2000).

RL

RL

[3]

RP

RP CHARACTERIZATION.

RX MEDLINE=86085936; PubMed=2867095;

RX

RA	Chandler C.J., Wang T.T., Halsted C.H.;
RH	"Pteroylpolyglutamate hydrolase from human jejunal brush borders.
RT	Purification and characterization.";
RL	J. Biol. Chem. 261:928-933(1986).
CC	-1- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-
CC	acidic dipeptide (NALADASE) activity. Has a preference for tri-
CC	alpha-glutamate peptides (By similarity). In the intestine,
CC	required for the uptake of folate. In the brain, modulates
CC	excitatory neurotransmission through the hydrolysis of the
CC	neuropeptide, N-acetylaspartylglutamate (NAAG), thereby releasing
CC	glutamate. Maximal activity at pH 6.0.
CC	-1- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity
CC	(By similarity). In vitro, cleaves Gly-Pro-Arm (By similarity).
CC	-1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC	glutamyl residue, typically from Ac-Asp-Glu or pteroyl gamma.
CC	-1- COFACTOR: zinc; Binds two ions per subunit. Required for NALADASE
CC	activity.
CC	-1- ENZYME REGULATION: The NALADASE activity is inhibited by
CC	quisqualic acid, beta-NAG and 2-(phosphomethyl) pentanedioic
CC	acid (PMAA). Ethanol ingestion decreases the folate hydrolase
CC	activity by 50%.
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane
CC	(By similarity).
CC	-1- TISSUE SPECIFICITY: High expression in the duodenum and in the
CC	jejunum brush-border membrane. Weak expression in kidney.
CC	-1- DOMAIN: The NALADASE activity is found in the central region, the
CC	dipeptidyl peptidase IV type activity in the C-terminal.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF050502; AAC39269.1; --
DR	MEROPS; M28.010; --
DR	InterPro; IPR003137; PA.
DR	Pfam; PF02225; PA; 1.
DR	Pfam; PF04389; Peptidase_M28; 1.
DR	Pfam; PF04253; TRF_dimer; 1.
KM	Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;
KW	Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
KW	Signal-anchor; Multifunctional enzyme.
FT	DOMAIN 1 19
FT	TRANSMEM 20 43
FT	-----
FT	DOMAIN 44 750
FT	DOMAIN 147 150
FT	DOMAIN 275 588
FT	ACT_SITE 425 425
FT	ACT_SITE 629 629
FT	ACT_SITE 667 667
FT	ACT_SITE 690 690
FT	ACT_SITE 378 378
FT	METAL 388 388
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FT	METAL 454 454
FT	METAL 554 554
FT	METAL 77 77
FT	CARBOHYD 122 122
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FT	CARBOHYD 196 196
FT	CARBOHYD 337 337
FT	CARBOHYD 460 460
FT	CARBOHYD 477 477
FT	CARBOHYD 614 614
FT	CARBOHYD 639 639
FT	CARBOHYD 646 646
FO	SEQUENCE 751 AA; 84523 MW; AAF7B3526328CCA CRC64;

[illegible]

Query Match	88.7%	Score 2066;	DB 1;	Length 752;
Best Local Similarity	87.1%	Pred. No. 8.4e-146;		
Matches 384;	Conservative 29;	Mismatches 28;	Indels 0;	Gaps 0

Qy	1	MGSGAPPSMRGSLKYSXNPGPTGNEFSTQKVMHJHSNTEVRINYVIGTLCGAVER	60
Db	311	MGSGAPDSMKGGLKPYRNVNPGFAGNFQKQKVKLHJHSNKYTRIINVIGTLCGAVER	370
Qy	61	DRYVILGHRDSDWVEGGIDPQSGAAVYHETVRSFCTLLKEGMRPRTILFASWDAEEFGL	120
Db	371	DRYVILGHRDRAVWFGGIDPQSGAAVYHEIVRTFCTLLKKKGMRPRTILFASWDAEEFGL	430
Qy	121	LGSTEMAEDNSRLLQERGVAYIINDSSIEGVNTRLVDCDPLMYSLYUNLJTELSPPDEGF	180
Db	431	LGSTEMAEDHSRLLQERGVAYIINDSSIEGVNTRLVDCDPLMHSLYUNLJTELSPPDEGF	490
Qy	181	EGKSLYESWTKSSPSPERFSGMRISIKLGSNDFEYFQORLGIASGRATYTKMNETNKEG	240
Db	491	EGKSLYDSMKRKSSTPERIGMRISIKLGSNDFEYFQORLGIASGRATYTKMKNKYSS	550
Qy	241	YPLHSHVYEIYELVEKFTDPMFKHLYAOYRGCAVFEELANSIYLPEDCRDYAVVLRKYA	300
Db	551	YPLHSHVYEIYELVEKFTDPMFKHLYAOYRGCAVFEELANSIYLPEDCQSAVVALKHA	610
Qy	301	DKIYNISMKHPOEKKYTSLSPDSLFSAVKNTEIATSKESERJODEDKSNPILRRMNQOL	360
Db	611	ETIYNISMNHOEKKAYISFDSLFSAYNNNTDVAASKNÖRLÖDDKSNPILRLINDOL	670
Qy	361	MLTERAFIDPLGLDRPEYRHHVYIAPSSHNKYAGESPFGIYDALDEDSKYVSPKAWGDY	420
Db	671	MYLERAFIDPLGLDRPPRYRHHIYAPSSHNKYAGESPFGIYDALFDINNKVDTSKAMEV	730
Qy	421	KRÖISVAAFYQAAAEITLSEV 441	
Db	731	KRÖISIAAFYQAAAEITLREV 751	

	RESULT	4
ID	FOH1_MOUSE	
AC	035409; G9DDC2;	
DT	28-FEB-2003 (Rel. 41, Created)	PRT; 752 AA

DT 28-FEB-2003 (Ref. 41, last annotation update)
DE Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate
DE carboxypeptidase) (mccp) (N-acetylated-alpha-linked acidic dipeptidase
DE 1) (NALADase I) (Pteroylpolgamma-glutamate carboxypeptidase)
DE 1) (Polygamma-glutamate carboxypeptidase) (PGCP) (Folate hydrolase
DE 1) (Prostate-specific membrane antigen homolog).
GN POLH OR MOPSM OR NALADI.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH SWISS; TISSUE=Brain;
RX MEDLINE=2107532; PubMed=11210180;
RA Biedel D.J., Pinto J.T., Tong W.P., Heston W.D.W.:
RT "Cloning, expression, genomic localization, and enzymatic activities
RT of the mouse homolog of prostate-specific membrane antigen/NALADase/
RT folate hydrolase.";
RL Mamm. Genome 12:117-123(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=2108560; PubMed=1121751;
RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Aachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojuno M., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked
CC acidic dipeptidase (NALADase) activity. Has a preference for tri-
CC alpha-glutamate peptides (by similarity). In the intestine,
CC required for the uptake of folate. In the brain, modulates
CC excitatory neurotransmission through the hydrolysis of the
CC neuropeptide, N-acetylaspartylglutamate (NAAG), thereby releasing
CC glutamate.
CC -1- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity
CC (by similarity). In vitro, cleaves Gly-Pro-AMC (by similarity).
CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
CC -1- COFACTOR: Zinc; Binds two ions per subunit. Required for NALADase
CC activity.
CC -1- ENZYME REGULATION: The NALADase and folate hydrolase activities
CC are inhibited by quinsqualic acid.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane
CC (by similarity).
CC -1- TISSUE SPECIFICITY: Expressed predominantly in the hippocampal
CC region of the brain and in kidney. Lower levels in the ovary,
CC testis and mandibular gland.
CC -1- DOMAIN: The NALADase activity is found in the central region, the
CC dipeptidyl peptidase IV type activity in the C-terminal.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC -1- CAUTION: There are amino acid differences between the sequence
CC shown in fig.1 (Ref.1) and the sequence deposited in the database
CC (AF026380). The sequence from fig.1 shows only 3 conflicts between
CC Ref.1 and Ref.2. These are at AA positions 141, 240 and 287.

GN MA1AD2
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=1121781;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Glassi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikido T., Pesole G., Quackenbush J.,
 Schirral L.M., Staudt F., Suzuki R., Tomita M., Wagner U., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,

```

RT      "Functional annotation of a full length mouse cDNA collection."
RL      Nature 409:685-690(2001).
CC      -I- FUNCTION: Has N-acetylated-alpha-linked-acidic dipeptidase
CC      (NALADase) activity (By similarity). Also exhibits a dipeptidyl-
CC      peptidase IV type activity. In vitro, cleaves Gly-Pro-AMC (By
CC      similarity).
CC      -I- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC      glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma-
CC      -I- COFACTOR: Zinc. Binds two ions per subunit. Required for NALADase
CC      activity (By similarity).
CC      -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC      -I- DOMAIN: The NALADase activity is found in the central region, the
CC      dipeptidyl peptidase IV type activity in the C-terminal.
CC      -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
-----
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CC      or send an email to license@sib-sib.ch).
CC
DR      EMBL: AK012270; BAB28132.1; -.
DR      MEROPS: M28.012; -.
DR      MGD: MGI:1919810; Nalad2.
DR      Pfam: PF04389; Peptidase_M28; 1.
DR      Pfam: PF04253; TFR_dimer; 1.
KW      Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;
KW      Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
KW      Signal-anchor; Multifunctional enzyme.
FT      NON_TER      1
FT      DOMAIN      1
FT      FT      <1      94      NALADASE.
FT      ACT_SITE      135      135      CHARGE RELAY SYSTEM (POTENTIAL).
FT      ACT_SITE      173      173      CHARGE RELAY SYSTEM (POTENTIAL).
FT      ACT_SITE      196      196      CHARGE RELAY SYSTEM (POTENTIAL).
FT      METAL      60      60      ZINC 1 (BY SIMILARITY).
FT      CARBOHYD      120      120      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      145      145      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      257 AA: 29081 MW: 1E090769099E50BA CRC64:
Query Match      39.3%; Score 916; DB 1; Length 257;
Best Local Similarity      66.5%; Pred. No. 5,2e-61;
Matches 167; Conservative 43; Mismatches 41; Indels 0; Gaps 0

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```
Db 6 EKDPSPENKPEPRNKGSSGSDPEAYFQRIQGIASGRKRYTKNKTDYSSYPVHTTYET 65
      :| ||| :|||:|||||:| :|||||:|||||:|:|:| :|||:||||
QY 251 YELVEKEYPDMFKYHLTAQVGRGMVELANSIVLPEDCRVAVLRKADKIYNISMKH 310
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 66 FELVQNYDDPFRKQSLQVADLRGALVELADSVIPEPINIDYAKALNYSAINISKH 125
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 311 PQEMKTVSLSPDLSFSAVKNFETASKFSERLQDPKSNPILRMNDQMLFERATDP 370
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 126 DQOLRNHNAVSDPLFSAVKNSEASDPFHRRLQVLDLNNPRAVRIMDQMLTERAFIDP 185
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 371 LGPDRFRRHYIYAPSSHKNKYAGESFPGIYDAFDIESKYDPSKANGDYKROISVAFT 430
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 186 LGPGRKFRFRIITPAPSSHNNKYAGESFPGIYDAFDIENKADPSLAWAEVAKHISIAFT 245
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
QY 431 VOAAAEFLSEV 441
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|
Db 246 IQAAAGTLTNV 256
      :|||: ||| :| :|||:| :|||:| :|||:| :|||:| :|||:|

RESULT 7
NDL_NL_RAT NDL_RAT STANDARD: PRT: 745 AA.
AC 054697:
DE 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE N-acetylated-alpha-linked acidic dipeptidase like protein
  (EC 3.4.17.21) (NALADase L) (Ileal dipeptidylpeptidase) (100 kDa
  ileum brush border membrane protein) (I100).
DE NALADL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague-Dawley; TISSUE=Ileum;
RX MEDLINE=98049571; PubMed=9388249;
RA Sheiderer B.L., Thevananthar S., Moyer M.S., Walters H.C., Rinaldo P.,
  Devarajan P., Sun A.Q., Dawson P.A., Ananthanarayanan M.;
  *Cloning and characterization of a novel peptidase from rat and human
  ileum.*;
RT J. Biol. Chem. 272:31006-31015(1997).
RL -1- FUNCTION: Has no NAAG hydrolyzing activity (By similarity).
      Exhibits a dipeptidyl-peptidase IV type activity. In vitro,
      cleaves Gly-Pro-AMC.
CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
      glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
CC -1- COFACTOR: Zinc. Binds two ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Ileal brush border
      membrane.
CC -1- TISSUE SPECIFICITY: Mainly expressed in the distal small
      intestine.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF009921; AAB87644.1; -
CC MEROPS: M28.011: -
DR InterPro: IPR003137; PA.
DR Pfam: PF04389; Peptidase_M28; 1.
DR Pfam: PF04253; TFR_dimer; 1.
KW Hydroxylase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;
  Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
  Signal-anchor; Multifunctional enzyme.
```

```
FT DOMAIN 1 6
FT TRANSSEM 7 28
FT FT
FT FT
FT DOMAIN 29 745
FT DOMAIN 268 584
FT DOMAIN 635 639
FT ACT_SITE 421 421
FT ACT_SITE 622 622
FT ACT_SITE 662 662
FT ACT_SITE 693 693
FT METAL 373 373
FT METAL 383 383
FT METAL 422 422
FT METAL 450 450
FT METAL 550 550
FT CARBOHYD 128 128
FT CARBOHYD 141 141
FT CARBOHYD 235 235
FT CARBOHYD 279 279
FT CARBOHYD 304 304
FT CARBOHYD 350 350
FT CARBOHYD 456 456
FT CARBOHYD 497 497
FT CARBOHYD 593 593
FT CARBOHYD 620 620
FT SEQUENCE 745 AA; 80640 MW; A59C2EPD33B36B5 CRC64;

Query Match 37.94; Score 882.5; DB 1; Length 745;
Best Local Similarity 40.94; Pred. No. 6.5e-58;
Matches 187; Conservative 97; Mismatches 140; Indels 33; Gaps 13;

QY 1 MGSAPPDSSWRGSLKYSYNGPGF--TGNF-STQXKMHHSNENYTRINYGLTIRGA 57
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 303 LNTGSAPD-SWQAGGEYKLGPGEPNGNPPAGESEKVSYNLELRNSSNVGLTIQGA 361
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 58 VEPDRYIILGGRHSWYFGGIDPQGAAVHEIYRSFGTLKES-WRPRTILFASMDAE 116
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 362 VEPDRYIYIGNHRHSWYHGAVDPSSGTRAVLIEIRVGLTKTKTWPRRSIIFASMGAE 421
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 117 EFGLLGSTEAMEDNSRLLOERGVAVINADSSIEGNYTLRVDCPLMYSLVYNLKELEKSP 176
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 422 EFGLLGSTEFEELSKLOERTVYINVDISVFSNATLRAGCTPPVQSVISARKETISAP 481
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 177 DEGEGRSLYSW---TKKSPSESGMPRIKSLGSGNDFEVFQRIQGIASGRARYTKNW 233
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 482 --GSSGLSIYDNMTRKYWRS-SPYVGLVPSMGLGASDYSVLFHFGITSMDLATY--Y 536
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 234 ETNPFSG--YPLYHSVYETVELKEFYDPMFKYHLTAQVGRGMVELANSIVLPFCORD 291
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 537 DRKTSARIITYTHATDTPYVEKFDPGSSHQNAVAKTAGSVILRLSDSLFPLNVSQ 596
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 292 YAVVLRYADKIYINISMKHPQ-----MKTVSLSPDLSFSAVKNFETASKFSERLQDFD 346
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 597 YSETLQSF-----LQAQENLGALLSHNISGLPLVTAVERKKAALNQHILTIQ 648
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 347 KS--NPILRMNDQMLFERAFIDPLGPRPRYRHYIYAPSSHNNKYAGESFPGIYDAL 404
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 649 KSSDPLQVRRVNDQMLMLERAFINPRAFPERRKYSIHLMP---NTASVATFPGLANAY 705
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 405 FDIESKVDPSKAMGDYKROISVAAFVVOAAEFLSEV 441
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 706 ARAQELNSGAEAMAEVEKQLSIAVMALEGAATIQPV 742
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 8
NDL_HUMAN NDL_HUMAN STANDARD: PRT: 740 AA.
AC Q9UQ01: Q43176;
DE 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE N-acetylated-alpha-linked acidic dipeptidase like protein
  (EC 3.4.17.21) (NALADase L) (Ileal dipeptidylpeptidase) (100 kDa
```

DE Iileum brush border membrane protein (I1100).
 GN MALADL OR MALADASEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
 RC TISSUE=Small Intestine;
 RX MEDLINE=99185063; PubMed=10085079;
 RA Pangalos M., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,
 RA van der Helm L., Fripiot E., Ashton D., Gordon R.D.;
 RT "Isolation and expression of novel human glutamate carboxypeptidases
 RT with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
 RT peptidase IV activity";
 RT J. Biol. Chem. 274:8470-8483(1999).
 RL [2]
 RP SEQUENCE OF 419-740 FROM N.A.
 RC TISSUE=Ileum;
 RX MEDLINE=98049571; PubMed=9388249;
 RA Shneider B.L., Thevananthar S., Moyer M.S., Walters H.C., Rinaldo P.,
 RA Devarajan P., Sun A.O., Dawson P.A., Ananthanarayanan M.;
 RT "Cloning and characterization of a novel peptidase from rat and human
 RT ileum";
 RL J. Biol. Chem. 272:31006-31015(1997).
 CC -1- FUNCTION: Nucleotase-like activity unknown. Has no NAAG hydrolyzing
 CC activity. Exhibits a dipeptidyl-peptidase IV type activity. In
 CC vitro, cleaves Gly-Pro-AMC (By similarity).
 CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
 CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
 CC -1- COFACTOR: Zinc. Binds two ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Ileal brush border
 CC membrane.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=8;
 CC Name=1;
 CC IsoId=Q9U0Q1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9U0Q1-2; Sequence=VSP_005343;
 CC Name=3;
 CC IsoId=Q9U0Q1-3; Sequence=VSP_005344;
 CC Name=4;
 CC IsoId=Q9U0Q1-4; Sequence=VSP_005345;
 CC Name=5;
 CC IsoId=Q9U0Q1-5; Sequence=VSP_005346, VSP_005347;
 CC Name=6;
 CC IsoId=Q9U0Q1-6; Sequence=VSP_005348, VSP_005349;
 CC Name=7;
 CC IsoId=Q9U0Q1-7; Sequence=VSP_005350, VSP_005351;
 CC Name=8;
 CC IsoId=Q9U0Q1-8; Sequence=VSP_005352, VSP_005353;
 CC -1- TISSUE SPECIFICITY: Mainly expressed in the distal small
 CC intestine. Also expressed in the spleen and testis. Weak
 CC expression in the brain, locating mainly to the brain stem,
 CC amygdala, thalamus and ventral striatum. Isoforms 2 and 3 are
 CC found in the small intestine and colon.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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 CC -----
 CC EMBL, AJ012371, CAB39968.1; -;
 CC EMBL, AF010141, AAB87645.1; -;
 CC MEROPS, M28. 011, -;
 CC MIM, 602640, -;
 CC InterPro: IPR003137, PA.
 CC Pfam, PF02225, PA, 1.
 CC Pfam, PF04389, Peptidase_M28, 1.
 CC

DR	PFam: PF04253; TFR dimer: 1.	
KM	Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;	
KM	Dipeptidase; Serine protease; Transmembrane; Glycoprotein;	
KM	Signal-anchor; Multifunctional enzyme; Alternative splicing.	
FT	DOMAIN 1 6	
FT	TRANSMEM 7 28	
FT	DOMAIN 29 740	
FT	DOMAIN 263 579	
FT	ACT_SITE 416 416	
FT	ACT_SITE 617 617	
FT	ACT_SITE 657 657	
FT	ACT_SITE 687 687	
FT	ACT_SITE 368 368	
FT	METAL 378 378	
FT	METAL 417 417	
FT	METAL 445 445	
FT	METAL 545 545	
FT	CARBOHYD 136 136	
FT	CARBOHYD 274 274	
FT	CARBOHYD 299 299	
FT	CARBOHYD 334 334	
FT	CARBOHYD 345 345	
FT	CARBOHYD 451 451	
FT	CARBOHYD 492 492	
FT	CARBOHYD 161 201	
FT	VARSPLIC 296 330	
FT	VARSPLIC 359 359	
FT	VARSPLIC 502 522	
FT	VARSPLIC 523 740	
FT	VARSPLIC 502 543	
FT	VARSPLIC 562 579	
FT	VARSPLIC 544 740	
FT	VARSPLIC 580 740	
FT	VARSPLIC 619 635	
FT	VARSPLIC 636 740	
FT	CONFLICT 420 424	
FT	SEQUENCE 740 AA; 80620 MW; 1	
QY	Query Match 37.1%; Score 863.5; DB 1; Length 740;	
QY	Best Local Similarity 40.1%; Pred. No. 1.7e-56;	
QY	Matches 185; Conservative 91; Mismatches 146; Indels 39; Gaps 13	
Db	1 MGGSAPDDSSWRGSLKSTVNVGPGF -TGNF-STQYKMMIHSTNEVTRYLYNIGTLRGA 57	
Db	298 LMGTLAT-ATWQAGLCHYRLGPGRPDPDPAQSVNVSVLLETRNSNVLGIIRGA 356	
QY	58 VEPDRVYLIGGRDSWVVGGLDPOGAVVHEVYRSGTLLKKE-WMPRTILFAADAE 116	
Db	357 VEPDRVYLKGNRDSWVGAVDPSSGIVLVLELSRVGLTKLKGTPMRNSIVFAWGAE 416	
QY	117 EFGILGSTEWMADNSRLLOEGRVAATINDSSIEENTYLRVDCPLMYSLVYNLTKEKSP 176	
Db	417 EFGILGSTEFTFEFPFNKLOEGRVAATINDISVPANATLRVQGTTPPVQSVFASMTKEIRSP 476	
QY	177 DGEFGKSLYESWTK-RKSPSEFGMRISKLGSDNDEVEFQRLGIASGARVYTKNME 234	

```
Db 477 GPG--DUSTINMTRREYENRSSPVGLVPSLGSILGASDYAPFVHFLGSSMDIAYT--YD 532
QY 235 TNKFSG--YPLLYHSVYETVELKEFYEDPMFKYHLTVAOVRCGMVFEELANSIVLPEDCDRY 292
Db 533 RSKTSARIPYPIYHAFIDFVDYDKFDLDPGFSHQAVARTAGSVILRLSDSFLLKXSDY 592
QY 293 AVYLKRAKADKTYINSMKHPOE----MKTVSLSPDSLFSAVKNFTETASKFESRLQDFDK 347
Db 593 SETLRSEF-----LQAAQODLGCALLEOHHSISLGPVTVAAVEKEFEAEKAAALGQRISTLOK 644
QY 348 S--PILLRMNDOLMFLERAFIDPLGDPDRFRRHYTAS-----SHNKYAGSFPCIX 401
Db 645 GSPPLQYRMLNDQMLLEKFTFLNPRAPFERRYTSHVLAAPSHELGRSH-----IPGLS 697
QY 402 DALFDIESKVDPSKAWGDYVKRQISVAAFVQAAEFTLSEVA 442
Db 698 NACSRARDTASGSEAWAEVQROSLSVTALGGAATLRPA 738

RESULT 9
GCP2_CAEEL STANDARD; PRT; 751 AA.
AC P91406:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate carboxypeptidase II homolog (EC 3.4.17.21).
GN R57.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2.
RA Favello A., Rifkin L., Chiapelli B.:
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
CC -1- COFACTOR: Zinc; Binds two ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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CC EMBL; U08179; AAB52660.1; -.
CC PIR; T30154; T30154.
DR MEROPS; M28.010; -.
DR WormPep; R57.1; CE12844.
DR InterPro; IPR00137; PA.
DR Pfam; PF04389; Peptidase_M28; 1.
DR Pfam; PF04253; TFR_dimer; 1.
KW Hypothetical protein; Hydrolase; Carboxypeptidase; Metalloprotease;
KW Zinc; Transmembrane; Glycoprotein; Signal anchor.
KW DOMAIN 1
FT TRANSMEM 7 23
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT CATALYTIC (BY SIMILARITY).
FT NUCLEOPHILE (BY SIMILARITY).
FT ZINC 2 (BY SIMILARITY).
FT ZINC 1 AND 2 (BY SIMILARITY).
FT ZINC 1 (BY SIMILARITY).
FT ZINC 2 (BY SIMILARITY).
FT ZINC 1 (BY SIMILARITY).
FT METAL 543 543
FT METAL 543 543
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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 587 587 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 751 AA; 83683 MW; 1A08AA4974FA2967 CRC64;

Query Match 27.1%; Score 631.5; DB: 1; Length 751;
Best Local Similarity 32.8%; Pred. No. 2.9e-39;
Matches 151; Conservative 101; Mismatches 168; Indels 41; Gaps 20;

QY 6 PDDSSWGSGL--KRYANVGQGFNTGNFSTOKYKMHHSSTNEYTRYNYIGTLRGAVEEDRY 63
Db 306 PAPSDMOGFVGGNLTLYLKGQFVNG---EKLSIVHSELKTRKIRNVTGYIRGSEEPDSY 362
QY 64 VILGHRDQWVFGGIDPQSGAAVYHETRS--FGTLKREGRMRPRTTLFASMDAEEFGILG 122
Db 363 IMGNHFDAMWYGSIDPNSGTAVLAEVARAMQGTINETSMPARTIYFNAMDAEEFGILG 422
QY 123 STEWAEENSRLLDGRGAYIINADSSIEGNTTLRYDCPLMYSLVYNTLTKELKSPD--EGF 180
Db 423 STEVEEFVNLIQKRAVYIINMD--CIQGNISLHVDPILEHVAIEAKSVENPSKRERS 481
QY 181 EG--KSLYESMTKRSPESEFGMPRIKSGNDPEVEFGRLGASGARAT--KNWETNKF 238
Db 482 RGRKTYLIDYMKKVPFDKK--AGVPRIVPGGSDHAPLNRAGVAV--INTEFNKYYT--W 536
QY 239 SGYPLYSVYET--VELKEFYEDPMFKYHLTVAOVRCGMVFEELANSIVLPEDCDRYA--VVL 296
Db 537 DTYPLHYTHYETPEPSNHLDTDNLVSKHAIQGYWAEMLATFADVDYTLPMNTJHFAFVVL 596
QY 297 RKYADKI-----YINSMKHPOEAKT--YSLSPDSLFSAVKNFTETASKFESERL----QDF 345
Db 597 KYLPQLKTTIGSLNRSDFEDIRTOYAL---LSKSADDLTMSKKFQETIHFTQHSF 652
QY 346 DKS--NPILLRMNDOLMFLERAFIDPLGPR--DRPFRRHYTAPSSHNKYAGSFPCIXD 402
Db 653 SQNPYDKHNAVNERKLSERECTINRGVSMNPASRAHLYFSVSDSSYSSSLMAGVON 712
QY 403 AL--FDIESKVDPSKAWGDYVKRQISVAAFVQAAEFTLSEV 441
Db 713 AINSYDLN---PTKKGLREIINQISIVQSVICVNTLRDV 750

RESULT 10
GCP2_ARATH STANDARD; PRT; 705 AA.
ID GCP2_ARATH
AC 09M158;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable glutamate carboxypeptidase II (EC 3.4.17.21).
GN AMP1 OR AT3G54720 OR T5N23.80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE-Siliques;
RX MEDLINE=21434423; Pubmed=11549767;
RA Hellmell C.A., Chin-Atkins A.N., Wilson I.W., Chapple R.,
RA Dennis E.S., Chaudhury A.:
RT "The Arabidopsis AMP1 gene encodes a putative glutamate
RT carboxypeptidase."
RL Plant Cell 13:2115-2125(2001).
RN [2]
RP SEQUENCE FROM N.A.
```


QY 408 ESKVDPKAMGVKROISVAFAFVQAAPETLS 439
 DB 769 ESR-----FRRLALITWTLGGANALIS 791

RESULT 12
 TFR2_MOUSE
 AC TFR2_MOUSE STANDARD: PRT: 798 AA.
 DT 09JRK3: 092016: 099M09: 09CPT2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 GN Transferrin receptor protein 2 (TFR2).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Embryo;
 RX MEDLINE=20160931; PubMed=10681454;
 RA Fleming R.E., Migas M.C., Holden C.C., Mahood A., Britton R.S.,
 RT "Transferrin receptor 2: Continued expression in mouse liver in the
 RL face of iron overload and in hereditary hemochromatosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2214-2219(2000).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Erythrocyte;
 RX MEDLINE=21426540; PubMed=11535534;
 RA Kawabata H., Germain R.S., Ikezoe T., Tong X., Green E.M.,
 RT "Regulation of expression of murine transferrin receptor 2.";
 RL Blood 98:1949-1954(2001).
 RN (3)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata Y., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Morone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (5)
 RP SEQUENCE OF 1-278 FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsai L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 CC -1- FUNCTION: Mediates cellular uptake of transferrin-bound iron in a
 CC non-iron dependent manner. May be involved in iron metabolism,
 CC hepatocyte function and erythrocyte differentiation.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Isoform 3 may be
 CC cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q9JRK3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9JRK3-2; Sequence=VSP_005357; VSP_005358;
 CC Note=lacks most of the extracellular domain. No experimental
 CC confirmation available;
 CC Name=3;
 CC IsoId=Q9JRK3-3; Sequence=VSP_005356;
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in liver. Also
 CC expressed in kidney, spleen, brain, lung, heart and muscle with
 CC very low expression in kidney, muscle and heart.
 CC -1- DEVELOPMENTAL STAGE: First expressed between embryo days 8 and 11.
 CC In the liver, expression increases during development from embryo
 CC day 13 to adulthood while, in the spleen, levels remain constant
 CC throughout development.
 CC -1- INDUCTION: Down-regulated during erythrocyte differentiation.
 CC Expression unchanged by cellular iron status.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF222895; AAF37272.1; -
 CC EMBL: AF207741; AAL05976.1; -
 CC EMBL: AF207742; AAL05977.1; -
 CC EMBL: AK004965; BAB23705.1; -
 CC EMBL: AK004848; BAB23614.1; -
 CC EMBL: BC013654; AAH13654.1; -
 CC EMBL: AF312033; AAK28830.1; -
 CC HSSP: P02786; 1CX8.
 CC MGD: MGI:1354956; Tfr2.
 CC InterPro: IPR003137; PA.
 CC Pfam: PF02225; PA; 1.
 CC Pfam: PF04389; Peptidase_M28; 1.
 CC Pfam: PF04253; TFR_dimer; 1.
 CC Transmembrane; Glycoprotein; Receptor; Signal-anchor;
 KW Alternative splicing
 FT DOMAIN 1 81 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 82 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).


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FT DOMAIN 103 798 EXTRACELLULAR (POTENTIAL).
FT SITE 23 26 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT DISULFID 106 106 INTERCHAIN (POTENTIAL).
FT CARBOHYD 109 109 INTERCHAIN (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 535 535 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VASPLIC 12 93 Missing (in isoform 3).
FT VASPLIC 237 237 /FtId=VSP_005356.
FT VASPLIC 237 237 T -> TVRFPGMAHHVIG (in isoform 2).
FT VASPLIC 238 798 /FtId=VSP_005357.
FT VASPLIC 238 798 Missing (in isoform 2).
FT VASPLIC 238 798 /FtId=VSP_005358.
FT CONFLICT 25 25 R -> P (IN REF. 2; AF207742).
FT CONFLICT 42 42 G -> V (IN REF. 2; AF207742 AND 5).
FT CONFLICT 103 103 R -> P (IN REF. 2; AF207742).
FT CONFLICT 151 151 T -> N (IN REF. 4).
FT CONFLICT 248 248 S -> L (IN REF. 2).
FT CONFLICT 287 287 A -> V (IN REF. 2).
FT CONFLICT 595 595 K -> E (IN REF. 1).
SO SEQUENCE 798 AA; 88402 MW; FA6161FE3FFE2AA4 CRC64;
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Query Match 19.6%; Score 457.5; DB 1; Length 798;
Best Local Similarity 27.4%; Pred. No. 2.6e-26;
Matches 125; Conservative 92; Mismatches 185; Indels 55; Gaps 14;
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QY 2 GGSAPPDSWMSGLKVS-YVNGPGFTGNFSTOKYKMHISTNEVTRYVIGTLCGAVEP 60
DB 368 GPVAPQE--WKGHLSGSPYRLGPG-----PDLRLVYNNNRVSTPLSNIFACLEGFAEP 418
QY 61 DRYVILGHRDVSFGGIDPOSGAAVYHEVYRSFGTLKKESGRRPRTILFASMDAEEFGL 120
DB 419 DRYVILGHRDVSFGGIDPOSGAAVYHEVYRSFGTLKKESGRRPRTILFASMDAEEFGL 478
QY 121 LGSTEMADNSRLQERGVAYINADSSIEGNYTLRVCTPLMYSLVYNLTRELKSPDEGF 180
DB 479 VGATEMELEGVLSHLKAAVYVSDNSVLGSGKHAHTSPILVLEILKQVSPNH-- 536
QY 181 EGKSLYESWTKKSPSPFGMPRISKSGNDPEVFQRLGIASGRARYTKMWTNFKFSG 240
DB 537 SGQRLYEQVALTHPSMAEVIQPLPMDSSASFTAF--ACVPAVEFSFMDDVY----- 588
QY 241 YPLVHSYETVELVEKYEDPMFKYHL-----TVAQVSGVWFELANSIVLPEDCRDIAVY 295
DB 589 YPFLHTKEDYENLHK-----MLRGRLLPAVVOVAQOLGILIRLSHDLPLDFGRYGDV 644
QY 296 LRYVADKIYNSMKHPQEMKTYSLSPDSIFSAVKNFELIASKFSERLQDPKSNPILIRM 355
DB 645 VLRIHIGNES-----GDLKERGLTLQWYSARQDYIRAAKELKKEIYSSERNDERLIRM 700
QY 356 MNDQMLFLERAFIDPLGLP-DRPFYRHVYVAPSSHNKYAGSPFGIYDALFDIESKYDPS 414
DB 701 YNVIMRVEFEFLSQVYSPADSPF-RHIFLGQGDH-----TLGALVDHLMML--RADGS 751
QY 415 KAMGD-----VKRQISVAFTVQAAETLS 439
DB 752 GAASSRLTAGLGFQESSRRRQLALLTWLTIOGAAANALS 788
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RESULT 13
TERL_RAT TERL_RAT STANDARD; PRT; 622 AA.
AC Q99376;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transferrin receptor protein 1 (TfR1) (TfR) (TfR) (TfR) (Fragment).
GN TfRc OR TfRf.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=91125359; PubMed=2126342;
RA Roberts K.P., Griswold M.D.;
RT "Characterization of rat transferrin receptor cDNA: the regulation of
RT transferrin receptor mRNA in testes and in Sertoli cells in culture.",
RL Mol. Endocrinol. 4:531-542(1990).
CC -I- FUNCTION: Cellular uptake of iron occurs via receptor-mediated
CC endocytosis of ligand-occupied transferrin receptor into
CC specialized endosomes. Endosomal acidification leads to iron
CC release. The apotransferrin-receptor complex is then recycled to
CC the cell surface with a return to neutral pH and the concomitant
CC loss of affinity of apotransferrin for its receptor. Transferrin
CC receptor is necessary for development of erythrocytes and the
CC nervous system (By similarity).
CC -I- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin
CC molecule per polypeptide chain (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
CC -I- TISSUE SPECIFICITY: In testis, expressed in Sertoli cells,
CC peritubular myoid cells and in germinal cells. Highest levels in
CC Sertoli cells.
CC -I- PTM: N- and O-glycosylated, phosphorylated and palmitoylated (By
CC similarity).
```

```
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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DR EMBL: M58040; AAA42273.1; -.
DR PIR: A34549; A34549.
DR HSSP: P02786; ICX8.
DR InterPro: IPR003137; PA.
DR Pfam: PF02225; PA; 1.
DR Pfam: PF04389; Peptidase_M28; 1.
DR Pfam: PF04253; TFR_dimer; 1.
KW Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
KW Signal-anchor; Endocytosis; Phosphorylation.
FT DOMAIN 1 1
FT SITE 431 622 LIGAND-BINDING (BY SIMILARITY).
FT SITE 508 510 CELL ATTACHMENT SITE (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 584 584 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 589 589 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SO SEQUENCE 622 AA; 70152 MW; 831E4FC16DE55703 CRC64;
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Query Match 19.1%; Score 445.5; DB 1; Length 622;
Best Local Similarity 26.0%; Pred. No. 1.5e-25;
Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;
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QY 1 MGSAPP-----DSSWRSGLKVSYVNGPGFTGNFSTOKYKMHISTNEVTRYVIGTLCG 56
DB 211 MEGNCPPSWNIDSSCK--LELSQN-----QWKLTVNNVNLKETRLINFEVIGK 257
QY 57 AVEPDRIYVILGHRDVSFGGIDPOSGAAVYHEVYRSFG-TLKKEGRRPRTILFASMDA 115
DB 258 YEEDPDIYVVGACDANGPGVAKSSVGTGLLKAQVFSIMSKDGRFSPRSIIFAFWTA 317
QY 116 EEFGLGSTEMADNSRLQERGVAYINADSSIEGNYTLRVCTPLMYSLVYNLTRELKSP 175
DB 318 GDVGAAPTEMLBESLHLKAFYTNLQKVYLGITNFKVASPFLTYLMGKIMQVVK 377
QY 176 PDEGFEKSKLY--ESWTKKSPSPFGMPRISKSGNDPEVFQRLGIASGRARYTKM 233
DB 378 P---IDKRYILRNSNWLSK-----IEELSLDMAFPFLYASGIDAVSPFCED- 422
QY 234 ETNKGSGYPLVHSYETVELVEKYEDPMFKYHLTVQAVRGVWFELANSIVLPEDCRDIA 293
```


Db 423 -----EDPPIGCTKLDYTEIILQKVPOLQWVRITAEVAGOPILIKTHDIELLLYEMYN 477
Oy 294 VYLKRYADKIYNISMKHPQEMKTYSLSPDSLSFAKNFELIASKFSERLODDKSNPILL 353
Db 478 SKLLSFMMDLNFK-----ADIKMDGLSLQWLTLSANGDFRATSRLLTDFHNEKTKRFYM 533
Oy 354 RMMNDQMLEFAFLDPLGLPDRPFYRHVYAPSSHN-----KYAGESPFIYDALF 405
Db 534 REINDRIKVEHNFILSPYVSPRESFPHIFMGSGSHLTLSALVENLRKRNKTARNEITLF 593
Oy 406 DIESKVDSSKMGDVKROISVAAFVQALETLS 439
Db 594 -----RNDLALATWTIOGVANALS 612
RESULT 14
TFRL_CANFA STANDARD; PRT: 770 AA.
AC 09GLD3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transferrin receptor protein 1 (TFRL) (TR) (Tfr) (Tfrf).
GN TFRC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21165299; PubMed=11264378;
RA Parker J.S.L., Murphy W.J., Wang D., O'Brien S.J., Parrish C.R.;
RT Canine and feline parvoviruses can use human or feline transferrin
receptors to bind, enter, and infect cells.";
RL J. Virol. 75:3896-3902(2001).
CC -1- FUNCTION: Cellular uptake of iron occurs via receptor-mediated
endocytosis of ligand-occupied transferrin receptor into
specialized endosomes. Endosomal acidification leads to iron
release. The apotransferrin-receptor complex is then recycled to
the cell surface with a return to neutral pH and the concomitant
loss of affinity of apotransferrin for its receptor. Transferrin
receptor is necessary for development of erythrocytes and the
nervous system (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin
molecule per polypeptide chain (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
CC -1- PMW: N- and O-glycosylated, phosphorylated and palmitoylated (By
similarity).
CC -1- MISCELLANEOUS: Canine and feline parvoviruses bind human and
feline transferrin receptors and use these receptors to enter and
infect cells.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.

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CC EMBL; AF297626; AAC24850.1; -
CC HSSP; P02786; 1CX8.
DR InterPro: IPR003137; PA.
DR Pfam; PF02225; PA. 1.
DR Pfam; PF04389; Peptidase_M28; 1.
DR Pfam; PF04253; Tfr_dimer; 1.
KW Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
KW Signal-anchor; Endocytosis; Phosphorylation.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 90 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT

FT DOMAIN 91 770
FT 579 770
FT SITE 20 23
FT SITE 61 64
FT SITE 656 658
FT LIPID 65 65
FT LIPID 70 70
FT MOD_RES 24 24
FT DISULFID 92 92
FT 101 101
FT CARBOHYD 107 107
FT CARBOHYD 261 261
FT CARBOHYD 327 327
FT CARBOHYD 384 384
FT CARBOHYD 732 732
FT CARBOHYD 737 737
SQ SEQUENCE 770 AA; 86649 MW; 871F8320A1E1345A CRC64;
Query Match 19.1%; Score 445.5; DB 1; Length 770;
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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2; TISSUE=Hematopoietic;
RA Trowbridge I.S., Domingo D.L., Thomas M.L., Chai A.;
Submitted (Jan-1991) to the EMBL/GenBank/DBJ databases.
RL

REFERENCE	AUTHORS
3	Shibata, K., Itoh, M., Aizawa, K., Nagoka, S., Sasaki, N., Carninci, P., Suni, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M., Ishii, Y., Ishikawa, T., Nakamura, T., Hata, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Ozawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, T., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Katsunawa, T., Saito, R., Kadoya, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Knehl, P., Lewis, S., Matsuo, Y., Nikaio, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stambli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baidarelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gestblom, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Maffionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saeki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whitlaker, C., Wilmberg, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 3003)
AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Katsunawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome-gsc.riken.go.jp/ , Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	Please visit our web site (http://genome-gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer 15' GAGGAGAGGAGCGCCGACATCTGGAATTTTTTTTTTTTTVN 3', cDNA was prepared by using thermostable thermo-activated reverse transcriptase

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 REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 Title
 High-efficiency full-length cDNA cloning
 JOURNAL
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99379253
 PUBMED
 10349636
 REFERENCE
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Title
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL
 Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE
 20499374
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 11042159
 REFERENCE
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 Title
 RIKEN Integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL
 Genome Res. 10 (11), 1757-1771 (2000)
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 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
 Quackenbush, J., Schiml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
 Hofmann, M., Hume, D. A., Kamliya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,

Toyo-oka, K., Wang, K.H., Welte, C., Whitaker, C., Wilming, L.,
 Wyszynski, B., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.,
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL 6 (bases 1 to 2948)
 REFERENCES 6
 Adachi, Y., Aizawa, K., Akimura, T., Arai, K., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, A.,
 Takeuchi, Y., Tanaka, K., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 Direct Submission
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gscl.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
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 Db 931 AGCAATGATAGCGCTTAATAGGATGGAATGAGAGGCTGTTGCTTCCAGTATTC 990
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 QY 481 TGTTCATCCAGTTGATCTATGATGACAGAGAGCTTCCAGAGAGAGAGAGAG 540
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 Db 991 TGTTCATCCAGTTGATCTATGATGACAGAGAGCTTCCAGAGAGAGAGAGAG 1050
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 QY 541 ACACAGATGATGAGCTGGAGAGAGCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 600
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 Db 1051 ACCCTTCGACAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
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 QY 601 TACTGGAACCTTTCTACACAAAAGTCAAGATGACATCCACTTACCAATGAGTAC 660
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 Db 1111 TGTTCGAACTTTCTACACAAAAGTCAAGATGACATCCACTTACCAATGAGTAC 1170
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 QY 661 GAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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 Db 1171 AAGAACTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1230
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 QY 721 TCTGGAGAGTCCAGGAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
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 Db 1231 TCTGGAGAGTCCAGGAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1290
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 QY 781 TGTTCATGAACTGTGAGAGCTTTGGAACACTGAAAGAGAGAGAGAGAGAGAGAG 840
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 QY 841 AAGAACTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 899
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 Db 1351 AAGAACTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1410
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 QY 1080 TTTATGAAAGTGGAGCTTAAAGAGTCTTCCAGAGTTCAGTGGATGCCAGAGATA 1139
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 Db 1591 TTTATGAAAGTGGAGCTTAAAGAGTCTTCCAGAGTTCAGTGGATGCCAGAGATA 1650
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 QY 1140 GCAAAATGGAGATGGAATGATTTGAGAGTCTTCCAGAGCTTGAATGCTTCAG 1199
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 QY 1260 ACAGTCTATGAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1319
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 Db 1771 ACAGTCTATGAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1830
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 QY 1320 ACCTCACTGCGCCAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1379
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 Db 1831 ACCTCACTGCGCCAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1890
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 QY 1380 TCCCTTTGATGTCAGATATGCTGTGATTTAAGAAAGATGCTGACAAAATGTATAC 1439
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Db 1891 TTCCCTTTGACCTGCCAAAGTTATGCTGTAGCTGTGAAGATATGCTAGACATATCTACA 1950
 QY 1440 ATATTTCTATGAACATCCACAGGAATGAAGACATATGATTCATTTGATTCACCTT 1499
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 Db 2011 TTTCTGTAGTAAAAATTTTACAGAAATGCTTCCAGATTCCAGGAGACCTCCAGGA 2070
 QY 1559 TTTGACAAAAGCAACCAATATGTTTGAAGATGATGATATCATCTCATGTTCTTGAA 1618
 Db 2071 TTTGACAAAAGCAACCAATATGTTTGAAGATGATGATATCATCTCATGTTCTTGAA 2130
 QY 1619 AGAGCATTTTATGATTCATGAGGTTTACAGACAGACCTTTTATAGACATGTCATAT 1678
 Db 2131 CGTGCATTCATTTGATTCATGAGGTTTACAGACAGACCTTTTATAGACATGTCATAT 2190
 QY 1679 GCTCCAGACGACCAACAAAGTATGACAGGAGGAGTCTTCCAGGAATTTATGATCTCTG 1738
 Db 2191 GCTCCAGACGACCAACAAAGTATGACAGGAGGAGTCTTCCAGGAATTTATGATGAGCTT 2250
 QY 1739 TTTGATTTTGAAGCAATGAGACCTTCCAGAGGCTGGGAGATGTTGAAGACATAT 1798
 Db 2251 TTTGATTTTGAAGCAATGAGACCTTCCAGAGGCTGGGAGATGTTGAAGACATAT 2310
 QY 1799 TCT-GTTCAGACCTTTCACAGTGCAGGAGCTGCAGAGACTTTGATGATGAGCT 1853
 Db 2311 TCTAGTTGCAACCTTTTACAGTGCAGGAGCTGCAGAGACTTTGATGATGAGCT 2366

RESULT 3
 AL532732 1201 bp mRNA linear EST 23-MAY-2003
 LOCUS AL532732 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DN001YK13 5-PRIME, mRNA sequence.
 ACCESSION AL532732
 VERSION AL532732.2 GI:31070564
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12796225.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5903.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DN001YK13&cluster=5903.r. Contact :
 Peng Liang Email: filiang@life.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DN001YK13

FEATURES
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 /clone="CS0DN001YK13"
 /tissue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."
 BASE COUNT 340 a 231 c 312 g 294 t 24 others
 ORIGIN
 Query Match 46.9%; Score 933.4; DB 9; Length 1201;
 Best Local Similarity 97.6%; Pred. No. 1.7e-116;
 Matches 973; Conservative 5; Mismatches 16; Indels 3; Gaps 3;

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 Db 75 AGGTTAAATATGCCACCTGCGAGGGGCGCAAGAGAGATCTTCTACTGACCCCTG 134
 QY 300 ACTACTTGTCTGCTGGGGAAGTCTATCCACAGAGGTTGAATCTTCTGAGAGTGTG 359
 Db 135 ACTACTTGTCTGCTGGGGAAGTCTATCCACAGAGGTTGAATCTTCTGAGAGTGTG 194
 QY 360 TCCAGCGTGAATATCTTAAATCTGAATGTGTGAGAGACCTCTCACACGATTACC 419
 Db 195 TCCAGCGTGAATATCTTAAATCTGAATGTGTGAGAGACCTCTCACACGATTACC 254
 QY 420 CAGCAATGATACGCTTATAGGCAATGAGAGGCTGTGGCTTCCAGATATTC 479
 Db 255 CAGCAATGATATGCTTATAGGCGTGAATGTGAGAGGCTGTGGCTTCCAGATATTC 314
 QY 480 CTGTTCATCCAGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 539
 Db 315 CTGTTCATCCAAATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 374
 QY 540 CACCACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 599
 Db 375 CACCACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 434
 QY 600 TTTACTGGAATCTTTTACACAAAGGTCGAAGTGCATCCCTGATCCAAATGAAGTGA 659
 Db 435 TTTACTGGAATCTTTTACACAAAGGTCGAAGTGCATCCCTGATCCAAATGAAGTGA 494
 QY 660 CGAATATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 719
 Db 495 CGAATATTTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
 QY 720 TTTGGGAGGTACACCGGAGCTCATGGGTGTTGGTATTTGAACCTCAGATGAGACAG 779
 Db 555 TTTGGGAGGTACACCGGAGCTCATGGGTGTTGGTATTTGAACCTCAGATGAGACAG 614
 QY 780 CTGTGTTCATGAAACGTGTGAGAGCTTTGGAACACTGAAAGGAGGTTGAGACCTA 839
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 QY 840 GAAGAACAATTTTGTGCAAGCTGGGATGAGAGATTTGGTCTTCTGTTCTACTG 899
 Db 675 GAAGAACAATTTTGTGCAAGCTGGGATGAGAGATTTGGTCTTCTGTTCTACTG 734
 QY 900 AGTGGGAGAGGATTAATCAAGACTCTTAAAGCGTGGCGTATTAATTAAGCTG 959
 Db 735 AGTGGGAGAGGATTAATCAAGACTCTTAAAGCGTGGCGTATTAATTAAGCTG 794
 QY 960 ACTCATTTAAGAAGGAAATACACTGTGAGGTGATTTTACACCACTGATATACAGCT 1019
 Db 795 ACTCATTTAAGAAGGAAATACACTGTGAGGTGATTTTACACCACTGATATACAGCT 854
 QY 1020 TGGTATACCACTTACAAAGAGCTGAAAGCCCTGATGAAGCTTTGAAGCAATCTC 1079
 Db 855 TGGTATACCACTTACAAAGAGCTGAAAGCCCTGATGAAGCTTTGAAGCAATCTC 914
 QY 1080 TTTATGAAAGTTGAGACTAAAAAGTCTTCCCAAGATTCAGTGCATGCCAGAGATTA 1139
 Db 915 TTTATGAAAGTTGAGACTAAAAAGTCTTCCCAAGATTCAGTGCATGCCAGAGATTA 974
 QY 1140 GCAATTTGGATGTGAAATGATTTTGAAGTCTTCCCAAGATTCAGTGCATGCCAGAG 1199
 Db 975 GCAATTTGGATGTGAAATGATTTTGAAGTCTTCCCAAGATTCAGTGCATGCCAGAG 1032
 QY 1200 GCAGAGCAGCGTATTAATAAATTTGGGAAACAACAA 1236

Db	1033 GC-GRACACGCTATCTACTAAATAATGGGACCAACACAA	1068
RESULT 4	AL563970	1201 bp
LOCUS	AL563970 Homo sapiens FETAL LIVER Homo sapiens CDNA clone	linear EST 31-MAY-2003
DEFINITION	CSODM001YE22 3-PRIME, mRNA sequence.	
ACCESSION	AL563970	
VERSION	AL563970.2	GI:31287955
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo..	
AUTHORS	1 (bases 1 to 1201)	
TITLE	Ll,W.B., Gruber,C., Jesse,J., and Polayes,D.	
JOURNAL	Full-length cDNA libraries and normalization	
COMMENT	Unpublished On Feb 15, 2001 this sequence version replaced g1:1291387. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5903.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSODM001BC1INP1&cluster=5903.r. Contact : Peng Liang Email : lliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paradise Avenue Genoscope sequence ID : CSODM001BC1INP1. Location/Qualifiers 1..1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODM001YE22" /tissue_type="FETAL LIVER" /dev_stage="fetal" /clone.lib="Homo sapiens FETAL LIVER" /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	
FEATURES	source	
BASE COUNT	342 a 251 c 212 g 333 t 63 others	
ORIGIN		
Query Match	45.2%; Score 900.4; DB 9; Length 1201;	
Best Local Similarity	92.2%; Pred. No.4.7e-112;	
Matches 1022; Conservative	29; Mismatches 47; Indels 11; Gaps 10;	
QY	844 AACATTTTGTTCGACGCTGGGATGCGAAGAAATTTGGTCTTGTGTTACTGAGTG 903	
DB	1101 AACACATTTTWTTRCATCTACGRTTCACAAAAATTTGTCTTC-TKGTTCTACGAGTG 1043	
QY	904 GCGAGGAGTAATTAATTAAGACCTCTTCAGAGCGTGGCGGCGCTTAATTAATGCTGACTC 963	
DB	1042 GWCAGGGGAGATTTCADG-CYCTCTTCAMGAGCGTGCGCKT-GCTTATATTAAGTCG-MBC 986	
QY	964 ATCTATAGAGAGAAATCTACACTCTGAGAGTGTATTGTA-CACACTGATGTACAGCTTGG 1022	
DB	985 ATCTATAG-ARGAACTACACTCTGTGAGTGTATTGTACACCGCGATGTACMGC-TKG 928	
QY	1023 TATACACCTAACAAAGAGCTGAAAAGCCCTGATGAGGCTTTGAAGCAATCTCTTT 1083	
DB	927 TACACAACTTAACAAAGGCTG-AAAGCCCTGATGAAGCTTTGAAGCAATCTCTTT 869	
QY	1083 ATGAAGTTGACTAAAAAAGCTCTCCCGAGAGTTGAGTGGAAGCCAGAGATAAGCA 1144	
DB	868 ATGAAGG-TGGAATTAATAAAGCTCTTCCCGAGAGTTGAGTGGAAGCCAGAGATAAGCA 810	

OY		1143	AATTGGGATCTGGAAATGATTTTGGAGTGTTCTTCACAGCACTTGGAAATGGCTCAGGCA	1202
Db		809	AATTGGGATCTGGAAATGATTTTGGAGTGTTCTTCACAGCACTTGGAAATGGCTCAGGCA	750
OY		1203	GAGCAGCGTACTCAAATAATGGGAACAACAATTCAGCGGCTATCCACTGTATCAC	1262
Db		749	GAGCAGCGTACTCAAATAATGGGAACAACAATTCAGCGGCTATCCACTGTATCAC	690
OY		1263	GTGTCATATGAACAATATAGAGTTGGTGGAAAAAGTTTTATGATCCAATGTTTTAAATATCACC	1322
Db		689	GTGTCATATGAACAATATAGAGTTGGTGGAAAAAGTTTTATGATCCAATGTTTTAAATATCACC	630
OY		1323	TCACTGTGGCCAGGTTGCAGAGGAGGATGCTGTTTAGAGCTAGGCCAATTCATAGTGGCTCC	1382
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OY		1383	CTTTTGATTTGTCGAGATTAATGCTGTACTTTTAAAGAATATGCTGCACAAAATCATACATA	1442
Db		569	CTTTTGATTTGTCGAGATTAATGCTGTACTTTTAAAGAATATGCTGCACAAAATCATACATA	510
OY		1443	TTTCTATGAACAATATCAGACAGGAATGAAGACATATACAGTTATATCATTTGACTTTT	1502
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OY		1503	CTGCAGTAAAAAATTTTATCAGAAATTCGCTCCAAAGTTTCAGCGAGAACACTCCAGACCTTTG	1562
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OY		1563	ACAAAGCAACCCCAATATTTGTTAAAGATGAATGATCACTCATGTTCTCGAAAGAG	1622
Db		389	ACMAAGCAACCCCAATATTTTAAAGATGAATGATCACTCATGTTCTCGAAAGAG	330
OY		1623	CATTATTTGATTCATTAGAGTTTACACAGACAGACCTTTTATAGSCATGTCATATGCTC	1682
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Db		209	ATATTGADKAGCTAWMTGTGTTCTTCCTCMWKKCTGGGGAGAAATGAAAGACAGATTTATG	150
OY		1803	TTGCAGCCCTTCACAGTCGACGAGCAGTCGACAGACACTTTGAGTGAATAGCCTTAAGAGATT	1862
Db		149	TTGCTGCCCTTCACAGTCGACGAGCCTGCTGCAGAGACTTTAGTGAATAGCCTTAAGAGATT	90
OY		1863	CTTTAGAGACCTCTGATTTGAATTTGTGTATGTCACTC--AAAGATAATATATGGGTA	1922
Db		89	CTTTAGAGACCTCTGATTTGAATTTGTGTATGTCACTCAGAAAGAAATCTTAATGGGTA	30
OY		1921	TATTTGATTAATTTTAAATTTGGTATATTT	1949
Db		29	TATTTGATTAATTTTAAATTTGGTATATTT	1
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LOCUS		AL532691	Homo sapiens ADULT BRAIN Homo sapiens cDNA clone	
DEFINITION		CS00M001XKJ3 3-PRIME, mRNA sequence.		
ACCESSION		AL532691		
VERSION		AL532691.2	GI:31070523	
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		1 (bases 1 to 1201)		
AUTHORS		Ii,W.B., Gruber,C., Jesse,J. and Polyes,D.		
TITLE		Full-length cDNA libraries and normalization		

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241 TAAAAATTTGGAGAAACAAACAAATTCAGCGGCTATCCACTGATCCAGAGTGTATGAAC 300
1276 ATATGAGTTGGTGGAAAAAGTTTATGATCCATTTTAAATATCAGCTCAGCTGGCCCA 1335
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301 ATATGAGTTGGTGGAAAAAGTTTATGATCCATTTTAAATATCAGCTCAGCTGGCCCA 360
1336 GGTTCGAGAGGAGGATGGTGTGAGTGGAGTCCAGTATCCATGATGCTCCCTTTGATGTCG 1395
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361 GGTTCGAGAGGAGGATGGTGTGAGTGGAGTCCAGTATCCATGATGCTCCCTTTGATGTCG 420
1396 AGATTATGCTGTACTTTTAAAGAAAGTATGCTGACAAATCTACATATTTCTATGAACA 1455
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421 AGATTATGCTGTACTTTTAAAGAAAGTATGCTGACAAATCTACATATTTCTATGAACA 480
1456 TCCACAGGAATTAAGACATTAACATTTATCATTTGATTCACCTTTTCTGACATGAACAA 1515
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481 TCCACAGGAATTAAGACATTAACATTTATCATTTGATTCACCTTTTCTGACATGAACAA 540
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541 TTTTACAGAAATTTGCTTCCAGAGTTCAGCGAGAGACCTCAGGACTTTGCAAAACCAACC 600
1576 AATATGTTAAGAAATGATGATGATCACTCATCTTCTGGAAGACATTTATTTGATTC 1635
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601 AATATGTTAAGAAATGATGATGATCACTCATCTTCTGGAAGACATTTATTTGATTC 660
1636 ATTATGCTTACACAGACATTTTATGAGCATGATCATCTTCTGGAAGACATTTATTTGATTC 1695
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661 ATTATGCTTACACAGACATTTTATGAGCATGATCATCTTCTGGAAGACATTTATTTGATTC 720
1696 CAATATGACAGAGGAGATCTTCCAGAGAAATTTATGATGCTCTGTTT-GATTTGAAGACA 1754
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721 CAATATGACAGAGGAGATCTTCCAGAGAAATTTATGATGCTCTGTTTGAATTTGAAGAAC 780
1755 AAGTGAACCTTCCAGAGGCTGGG--GAGATGTGAAGAGACAGATTTCTGTTGACGCT 1811
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781 AAGTGAACCTTCCAGAGGCTGGGAGAAATTAAGAGACAGATTTAATTTGATGACGCT 840
1812 T--CAGAGTGAAGCAGCTCAGAGAC-TTGGAGTTGAAGTACC 1852
841 TTCCAGTGAAGCAGCTCAGAGAC-TTGGAGTTGAAGTACC 884

RESULT 8
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DEFINITION R5127570 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG208080
VERSION BG208080.1 GI:13729767
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 776)
REFERENCE Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Kikla,A., Hess,J., Coltrien,K., Lo,K., Offenbacher

J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
MEDLINE
PUBMED
11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com
High quality sequence stop: 453.
Location/Qualifiers
1..776
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/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_id="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
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Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 230 a 157 c 127 g 262 t
ORIGIN
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Best Local Similarity 99.1% Pred. No. 6.2e-92;
Matches 766; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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AUTHORS	AI672408	690 bp	mRNA	linear	EST	07-MAR-2000					
TITLE	AI672408	690 bp	mRNA	linear	EST	07-MAR-2000					
JOURNAL	AI672408	690 bp	mRNA	linear	EST	07-MAR-2000					
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Db	Accession	Version	Keywords	Source	Organism	Reference Authors Title Journal Comment
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Db	1584	TAAAGATGATGAATGATCAACTCATGTTTTCGAAAGAGCATTTATTGATCCATTAGGCT	1643			
Db	392	TAAAGATGATGAATGATCAACTCATGTTTTCGAAAGAGCATTTATTGATCCATTAGGCT	333			
Db	1644	TACCAGACAGACCTTTTATTAGCATGTCATCTATGCTCCAGACGACCACACAGATATG	1703			
Db	332	TACCAGACAGACCTTTTATTAGCATGTCATCTATGCTCCAGACGACCACACAGATATG	273			
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Db	272	CAGGGAGATCATTTCCAGAGAAATTTATGATGCTGCTTTGATATGAAAGCAATGAGACC	213			
Db	1764	CTTCCAAAGGCTGGGGAGATGATGAAGACAGATTTCTGTTGCGACCTTCACAGTGCAGG	1823			
Db	212	CTTCCAAAGGCTGGGGAGATGATGAAGACAGATTTATGTTGCGACCTTCACAGTGCAGG	153			
Db	1824	CAGCTGCAGACCTTTGATGATGAGTATGAGAGATTTCTTTAGAGACTCTGATTTGAA	1883			
Db	152	CAGCTGCAGACCTTTGATGATGAGTATGAGAGATTTCTTTAGAGAACTCCGATTTGAA	93			
Db	1884	TTTGTGTGCTATGTCACATC--AAGCAATTAATAAGGATATATGATTAATTTAAATTTG	1941			
Db	92	TTTGTGTGCTATGTCACATC--AAGCAATTAATAAGGATATATGATTAATTTAAATTTG	33			
Db	1942	GTATATTTGAATTAAGTTGAATTTGAATTTATATAT	1973			
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ACCESSION	CA488428					
VERSION	CA488428.1	GI:24950277				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	1 (bases 1 to 916)					
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/ .					
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)					
	Unpublished					
	Contact: Robert Strausberg, Ph.D.					
	Email: cgapbs-remail.nih.gov					
	Tissue Procurement: Kristl A. Eglund, Ira Pastan					
	cDNA Library Preparation: Invitrogen Corp					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
	DNA Sequencing by: Agencourt Bioscience Corporation					
	Clone distribution: MGC clone distribution information can be					
	found through the I.M.A.G.E. Consortium/LNL at:					
	http://image.lnl.gov					
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QY 1688 AGCCACACAGATATGACGGGAGTCATCCACAGAAATTATGATGCTGCTTGATATT 1747
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Search completed: October 4, 2003, 20:55:20
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 4, 2003, 10:14:18 ; Search time 9490 Seconds

(without alignments)
8587.142 Million cell updates/sec

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Perfect score: 1992
Sequence: 1 agcaatactactaccacca.....taaaaaaaaaaaaaaaaaa 1992

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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41: em_hgtgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1702.6	85.5	2653	6	AX337498 Sequence
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4	1702.6	85.5	2653	6	I23794 Sequence 1
5	1702.6	85.5	2653	6	M99487 Human prost
6	1690.6	84.9	2518	9	AX176574 Homo sapi
7	1687.2	84.7	2558	6	AX376036 Sequence
8	1584	79.5	2253	6	AX467227 Sequence
9	1582.4	79.4	2253	9	AY101595 Homo sapi
10	1511.4	75.9	2472	9	BC025672 Homo sapi
11	1412.4	70.9	2061	6	AX403107 Sequence
12	1371.6	68.9	2532	4	AF050502 Sus scrofa
13	1263.6	63.4	2899	10	RNU75973
14	1257.2	63.1	2348	10	AF040256
15	1254.4	63.0	2259	10	AF513486 Rattus no
16	1251.8	62.8	2603	10	AF026380 Mus muscu
17	1084.8	54.5	1428	10	AF039707 Rattus no
18	885.4	44.4	3171	6	AX136153 Sequence
19	885.4	44.4	3171	6	BD123529 Secretory
20	885.4	44.4	3171	9	AK075390 Homo sapi
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22	883.8	44.4	3152	9	HSN012370 Homo sapi
23	860.6	43.2	2690	10	AY243507
24	684.6	34.4	2431	5	BC049312 Dantio rer
25	561.2	28.2	710	9	AF027824 Homo sapi
26	428	21.5	13788	2	AP003122 Homo sapi
27	428	21.5	19268	2	AC024234 Homo sapi
28	423.2	21.2	40131	2	AC136711 Homo sapi
29	412	20.7	93525	9	AF007544 Homo sapi
30	410.4	20.6	156255	2	AF002369 Homo sapi
31	410.4	20.6	157527	9	AC117746 Homo sapi
32	410.4	20.6	158524	2	AL162372 Homo sapi
33	410.4	20.6	187529	9	AC118273 Homo sapi
34	410.4	20.6	246865	2	AC074003 Homo sapi
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38	290.8	14.6	156255	2	AP002369 Homo sapi
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42	220.2	11.1	231	6	AX106673 Sequence
43	220.2	11.1	231	6	AX140964 Sequence
44	220.2	11.1	231	6	AX200824 Sequence
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ALIGNMENTS

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DEFINITION Homo sapiens prostate-specific membrane antigen-like protein
(PSMA/GCP III) mRNA, complete cds.
ACCESSION AF261715
KEYWORDS AF261715.1 GI:11078563
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1992)
O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.
TITLE Cloning and Characterization of a novel glutamate-prefering

Pred. No. is the number of results predicted by chance to have a

peptidase that maps to the SCZDII locus: a candidate gene for Schizophrenia?

JOURNAL
REFERENCE
AUTHORS
TITLE

Unpublished
2 (bases 1 to 1992)
O'Keefe,D.S., Baclich,D.J. and Heston,W.D.W.
Expression Profile of Prostate-Specific Membrane Antigen (PSMA) Versus a Prostate-Specific Membrane Antigen-Like Gene in Normal Tissues, Prostate Cancer and Tumor Associated-Vasculature

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unpublished
3 (bases 1 to 1992)
O'Keefe,D.S., Baclich,D.J. and Heston,W.D.W.
Direct Submission

Submitted (27-APR-2000) Cancer Biology, Cleveland Clinic Foundation, NB 40, 9500 Euclid Avenue, Cleveland, OH 44195, USA

FEATURES
source

1. 1992

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527..1855

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BASE COUNT 638 a 352 c 451 g 551 t

ORIGIN

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 QY 1981 AAAAAAAAAA 1992
 Db 1981 AAAAAAAAAA 1992

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 VERSION AX337498.1 GI:18128217
 KEYWORDS
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 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D. R. and Weaver, Z.
 TITLE Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 8007 13-DEC-2001;
 Avalon Pharmaceuticals (US)

FEATURES
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 ORIGIN

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 QY 300 ACTACTTTGCTCCGGGGTGAATGCTTATCCAGAGGTTGGAAATCTTCCGAGAGTGTG 359
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 Db 959 ACTACTTTGCTCCGGGGTGAATGCTTATCCAGAGGTTGGAAATCTTCCGAGAGTGTG 1018
 QY 360 TCCAGGCTGGAATATCTTAAATCTGAATGCTGAGAGAGACCTCTCACACAGGTTACC 419
 Db 1019 TCCAGGCTGGAATATCTTAAATCTGAATGCTGAGAGAGACCTCTCACACAGGTTACC 1078
 QY 420 CACCAATGATACGCTTATAGGCTGAAGATTCAGAGGCTGTGCTTCCAAATATTC 479
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1079 CACCAATGATATGCTTATAGGCTGAAGATTCAGAGGCTGTGCTTCCAAATATTC 1138
 QY 480 CTGTTCATCCAGTTGATTAATGATGACAGAGGCTCTTGAAGAAATGGTGGCTCAG 539
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1139 CTGTTCATCCAAATTTGATTAATGATGACAGAGGCTCTTGAAGAAATGGTGGCTCAG 1198
 QY 540 CACCACAGATACAGCTGGAGAGAGAGTCTCAAAGTGTCTCAATGTTGACCTGGCT 599
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1199 CACCACAGATACAGCTGGAGAGAGAGTCTCAAAGTGTCTCAATGTTGACCTGGCT 1258
 QY 600 TTACTGGAACCTTTTCTACACAAAAGTCAAGATGCATCCACTTACCAATGAAGTGA 659
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1259 TTACTGGAACCTTTTCTACACAAAAGTCAAGATGCATCCACTTACCAATGAAGTGA 1318
 QY 660 CGAGAAATTCATGATGATAGTACTCTCAGAGAGAGATGGAACGACAGATATGTCA 719
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1319 CAAGAAATTCATGATGATAGTACTCTCAGAGAGAGATGGAACGACAGATATGTCA 1378
 QY 720 TTCTGGAGAGTCAACGGGAGCTCATGGGTTGTTGGTATTTGACCTCAGAGTGGAG 779
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1379 TTCTGGAGAGTCAACGGGAGCTCATGGGTTGTTGGTATTTGACCTCAGAGTGGAG 1438
 QY 780 CTGTGTTTCAATGAACTGTGAGAGAGCTTTGGAACTGAAGAAAGAGGTTGAGACCTA 839
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1439 CTGTGTTTCAATGAAATTTGTGAGAGAGCTTTGGAACTGAAGAAAGAGGTTGAGACCTA 1498
 QY 840 GAAGAAATTTGTTGCAAGCTGGGATGCAAGAAATTTGCTCTGTTGTTCACTG 899
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1499 GAAGAAATTTGTTGCAAGCTGGGATGCAAGAAATTTGCTCTGTTGTTCACTG 1558
 QY 900 AGTGGCAGAGATTAATTCAGAGCTCTTCAAGAGCTGCGCTTATATTAATGCTG 959
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1559 AGTGGCAGAGATTAATTCAGAGCTCTTCAAGAGCTGCGCTTATATTAATGCTG 1618
 QY 960 ACTCATCTATAGAGAACTACACTGTGAGAGTTGATTTGATACCACTGATGTACAGCT 1019
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1619 ACTCATCTATAGAGAACTACACTGTGAGAGTTGATTTGATACCACTGATGTACAGCT 1678
 QY 1020 TGGTATACAACTTACAAAGAGCTGTAAGAGCTGATGAAGCTTTGAAGGCAATCTC 1079
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1679 TGGTATACAACTTACAAAGAGCTGTAAGAGCTGATGAAGGCAATCTC 1138
 QY 1080 TTTATGAAAGTTGAGCTTAAAGAAAGTCTTCCCAAGTTCACATGCGATCCAGAGTAA 1139
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1739 TTTATGAAAGTTGAGCTTAAAGAAAGTCTTCCCAAGTTCACATGCGATCCAGAGTAA 1198
 QY 1140 GCAAAATTTGGAGTCTGAATGATTTTGGAGTGTCTTCCAAAGCTTGAATGCTTCAG 1199
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1799 GCAAAATTTGGAGTCTGAATGATTTTGGAGTGTCTTCCAAAGCTTGAATGCTTCAG 1858
 QY 1200 GCAGAGCAGGTTACTTAAAGAAATTTGGGAAACAAATTCACGGCTATCCACTATTC 1259
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1859 GCAGAGCAGGTTACTTAAAGAAATTTGGGAAACAAATTCACGGCTATCCACTATTC 1918
 QY 1260 ACAGTCTATGAAACATATGATGAGTGTGGAAGATTTTATGATTCATGTTTAAATATTC 1319
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1919 ACAGTCTATGAAACATATGATGAGTGTGGAAGATTTTATGATTCATGTTTAAATATTC 1378
 QY 1320 ACCTACGTTGGCCAGGTTTCAGAGAGAGATGTTTGAAGCTTATCCATATGCTG 1379
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1979 ACCTACGTTGGCCAGGTTTCAGAGAGAGATGTTTGAAGCTTATCCATATGCTG 2038

OY		1202	TGGATATCAACCTTACAAAAGGCTGAAAGCCCTGTATTGAAGCCTTTGAAGGCAAATCTC	1079
Db		1679	TGGATACAACTTAACAAAAAGCGTGAAAAGCCCTGTATGAAGCGCTTTGAAGGCCAAATCTC	1738
OY		1080	TTTTATGAAACTTGGACTATAAAAAAAGTCCTTCCAGAGTTTCAGTGGCATGCCAGATTA	1139
Db		1739	TTTTATGAAAGTTGGACTATAAAAAAAGTCCTTCCAGAGTTTCAGTGGCATGCCAGATTA	1798
OY		1140	GCAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAACGACTTGGAAATGCTTCAG	1199
Db		1799	GCAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAACGACTTGGAAATGCTTCAG	1858
OY		1200	GCAGAGCACGCTATACTATAAAATTTGGAAACAAACAATTCAGGGCTATCCACTGATTC	1259
Db		1859	GCAGAGCACGCTATACTATAAAATTTGGAAACAAACAATTCAGGGCTATCCACTGATTC	1918
OY		1260	ACAGTGTCTATGAAACATATGAGTGTGGTGGAAAAAGTTTATGATCATGCTTAAATATTC	1319
Db		1919	ACAGTGTCTATGAAACATATGAGTGTGGTGGAAAAAGTTTATGATCATGCTTAAATATTC	1978
OY		1320	ACCTCACTGTGGCCCGCAGGTTCCGAGAGGAGTGTGTTTGAAGCTAACCAATTCATAGTC	1379
Db		1979	ACCTCACTGTGGCCCGCAGGTTCCGAGAGGAGTGTGTTTGAAGCTAACCAATTCATAGTC	2038
OY		1380	TCCTTTTGAATGTGCGAGATTAATGCTGTAGTTTAAABAAAGTATGCGACAAATCTTACA	1439
Db		2039	TCCTTTTGAATGTGCGAGATTAATGCTGTAGTTTAAABAAAGTATGCGACAAATCTTACA	2098
OY		1440	ATATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACCTT	1499
Db		2099	GTATTTCTATGAAACATCCACAGGAAATGAAGACATACAGTTTATCATTTGATTCACCTT	2158
OY		1500	TTTCTGCAATTAATAATTTTACAAATTTGCTTCCAAGTTTCAGGAGAAGACTCCAGACT	1559
Db		2159	TTTCTGCAATTAATAATTTTACAAATTTGCTTCCAAGTTTCAGGAGAAGACTCCAGACT	2218
OY		1560	TTGCAAAAGCAACCACATATTTGTTAAGATGATGAATGATCACTGATGTTCTGGAAA	1619
Db		2219	TTGCAAAAGCAACCACATATTTGTTAAGATGATGAATGATCACTGATGTTCTGGAAA	2278
OY		1620	GAGCATTTATTCATCTTAGGGTTTACACAGACAGCTTTTATATAGGCATGTCATATG	1679
Db		2279	GAGCATTTATTCATCTTAGGGTTTACACAGACAGCTTTTATATAGGCATGTCATATG	2338
OY		1680	CTCCAAGCAGCCACAAAGATATCTCAGGGAGTCAITTTCCAGGAATTTATGATCTCTGT	1739
Db		2339	CTCCAAGCAGCCACAAAGATATCTCAGGGAGTCAITTTCCAGGAATTTATGATCTCTGT	2398
OY		1740	TTGATATTTGAAAGCAAAAGTGGACCTTCCAAAGCCTGGGGAGTGAAGAGACAGATTT	1799
Db		2399	TTGATATTTGAAAGCAAAAGTGGACCTTCCAAAGCCTGGGGAGTGAAGAGACAGATTT	2458
OY		1800	CTGTGTGACGCTTCACAGTGCAGGACAGCTGCAGAGACTTTGATGTAAGTACCTTAAGAG	1859
Db		2459	ATGTTTGCAGCCTTCACAGTGCAGGACAGCTGCAGAGACTTTGATGTAAGTACCTTAAGAG	2518
OY		1860	ATTCTTTTAGAGACTCTGATTTGAATTTTGTGTGATGTCACTC--AAAAGATATATATGG	1917
Db		2519	ATTCTTTTAGAGAAATCCGATTTGAATTTTGTGTGATGTCACTC--AAAAGATATATATGG	2578
OY		1918	GTATATTTGATTAATTTTAAATTTGATTAATTTGAATTAAGTGAATATTTATATATATAA	1977
Db		2579	GTATATTTGATTAATTTTAAATTTGATTAATTTGAATTAAGTGAATATTTATATATATAA	2638
OY		1978	AAAAAAAAAAAAAAAAA 1992	
Db		2639	AAAAAAAAAAAAAAAAA 2653	
RESULT 4				
LOCUS		123794	2653 bp DNA linear PAT 07-Oct-1996	

DEFINITION	Sequence 1 from patent US 5538866.
ACCESSION	I23794
VERSION	I23794.1 GI:1603664
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2653)
TITLE	Israeli,R.S., Heston,W.D.W. and Fair,W.R.
JOURNAL	Prostate-specific membrane antigen
FEATURES	Patent: US 5538866-A 1 23-Jul-1996;
	Location/Qualifiers
	1..2653
BASE COUNT	782 a 524 c 640 g 707 t
ORIGIN	
Query Match	85.5%; Score 1702.6; DB 6; Length 2653;
Best Local Similarity	98.5%; Pred. No. 0;
Matches 1729; Conservative	0; Mismatches 24; Indels 2; Gaps 1;
QY	240 AGGTTAAATATGCCAGCTGGCAGGGGCCAAAGAGATCTTCTACTCAGACCCCTGCTG 299
Db	
	899 AGGTTAAATATGCCAGCTGGCAGGGGCCAAAGAGATCTTCTACTCAGACCCCTGCTG 958
QY	300 ACTACTTTGCTCCCGGGGTGAAGTCATCCAGACGGTTGGAAATCTTCCTGGAGGTGGT 359
Db	
	959 ACTACTTTGCTCCCGGGGTGAAGTCATCCAGATGGTTGGAAATCTTCTGGAGGTGGT 1018
QY	360 TCCAGCGGTGAATATCCTAAATCTGAATGGTGCAGAGACCCCTCACAACAGGTTACC 419
Db	
	1019 TCCAGCGGTGAATATCCTAAATCTGAATGGTGCAGAGACCCCTCACAACAGGTTACC 1078
QY	420 CAGCAATATGATACGCTTATATGCGATGGAAATGTCAGAGCGCTGTGGCTTCCAGATATTC 479
Db	
	1079 CAGCAATATGATACGCTTATATGCGATGGAAATGTCAGAGCGCTGTGGCTTCCAGATATTC 1138
QY	480 CTGTTTCATCCAGTTGGATCTATGATGACACAGAAGCTCTAGAAAAATGGGTGGCTCAG 539
Db	
	1139 CTGTTTCATCCAGTTGGATCTATGATGACACAGAAGCTCTCTGAAAAATGGGTGGCTCAG 1198
QY	540 CACCACCGATAGAGAGCTGGAGGAAAGTCTCAAAGTGTCTTACATGTTGGACCTGGCT 599
Db	
	1199 CACCACCGATAGAGAGCTGGAGGAAAGTCTCAAAGTGTCTTACATGTTGGACCTGGCT 1258
QY	600 TTACTGGAACCTTTCTTACACAAAAAGTCAAAGATGCACATCTCACTACCAATGAATGA 659
Db	
	1259 TTACTGGAACCTTTCTTACACAAAAAGTCAAAGATGCACATCTCACTACCAATGAATGA 1318
QY	660 CGAGAAATTTAATGTGATAGTACTCTCAGAGAGAGAGTGGAAACCGACAGATATGTCA 719
Db	
	1319 CAGAAATTTAATGTGATAGTACTCTCAGAGAGAGAGTGGAAACCGACAGATATGTCA 1378
QY	720 TTCTGGAGGTACACCGGACCTCATGGGTGTTGTGGTATTGACCTCAAGTGGACAG 779
Db	
	1379 TTCTGGAGGTACACCGGACCTCATGGGTGTTGTGGTATTGACCTCAAGTGGACAG 1438
QY	780 CTGTGTTTCATGAAGACGTGAGAGCTTTGGAACACATGAAAAAGAGGGGTGGAGACCTA 839
Db	
	1439 CTGTGTTTCATGAAGACGTGAGAGCTTTGGAACACATGAAAAAGAGGGGTGGAGACCTA 1498
QY	840 GAAGAACAAATTTGTTTTCAGAGCTGGGATGAGAGAAATTTGCTTCTTGGTCTACTG 899
Db	
	1499 GAAGAACAAATTTGTTTTCAGAGCTGGGATGAGAGAAATTTGCTTCTTGGTCTACTG 1558
QY	900 AGTGGGCGAGAGATTAATTCAGAGCTCCTTCAAGAGCGTGGCGTCTTAATTAATCTG 959
Db	
	1559 AGTGGGCGAGAGATTAATTCAGAGCTCCTTCAAGAGCGTGGCGTCTTAATTAATCTG 1618
QY	960 ACTCATCTATGAAGAGAACTACACTCTGAGAGTGAATTTGATGACCACTGATGTACAGCT 1019
Db	
	1619 ACTCATCTATGAAGAGAACTACACTCTGAGAGTGAATTTGATGACCACTGATGTACAGCT 1678

QY	1020	TGCTATCAACCTACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAAGGCAATCTC	1079
DB	1679	TGGACACAACTACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAAGGCAATCTC	1738
QY	1080	TTTATGAAGTGGACATAAAAAGCTCTCCAGAGTTCAGAGGATGGCCAGGATTA	1139
DB	1739	TTTATGAAGTGGACATAAAAAGCTCTCCAGAGTTCAGAGGATGGCCAGGATTA	1798
QY	1140	GCAAAATGGGATCGGAAATGATTTTGGAGTGTCTTCCAAAGCATTGGAATTCCTCAG	1199
DB	1799	GCAAAATGGGATCGGAAATGATTTTGGAGTGTCTTCCAAAGCATTGGAATTCCTCAG	1858
QY	1200	GCAGAGCAGGTATACATAAAATTTGGGAACAAACAAATTCAGGGCTATCCATGATTC	1259
DB	1859	GCAGAGCAGGTATACATAAAATTTGGGAACAAACAAATTCAGGGCTATCCATGATTC	1918
QY	1260	ACAGTGTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	1319
DB	1919	ACAGTGTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	1978
QY	1320	ACCTCACTGTGGCCAGGTTTCGAGAGGAGATGTGTTTGGCTAGCCAAATTCATAGTGC	1379
DB	1979	ACCTCACTGTGGCCAGGTTTCGAGAGGAGATGTGTTTGGCTAGCCAAATTCATAGTGC	2038
QY	1380	TCCCTTTGATGTGCGAGATTATCTGATGTTTAAAGAAATGATGCGACAAATCTACA	1439
DB	2039	TCCCTTTGATGTGCGAGATTATCTGATGTTTAAAGAAATGATGCGACAAATCTACA	2098
QY	1440	ATATTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	1499
DB	2099	ATATTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	2158
QY	1500	TTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAAAGTTCAGGAGAGCTCAGAGACT	1559
DB	2159	TTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAAAGTTCAGGAGAGCTCAGAGACT	2218
QY	1560	TTGCAAAAGCAACCCATATTTGTAAGAATGATGAATGATCACTCATGTTCTGGA	1619
DB	2219	TTGCAAAAGCAACCCATATTTGTAAGAATGATGAATGATCACTCATGTTCTGGA	2278
QY	1620	GAGCATTTATGATTCATTAGGTTTACAGACAGACCTTTTATAGCATGATCTATG	1679
DB	2279	GAGCATTTATGATTCATTAGGTTTACAGACAGACCTTTTATAGCATGATCTATG	2338
QY	1680	CTCCAAGCAGCCACAAAGATGAGGAGGAGTCACTTCCAGGAATTTATGATCTCTGT	1739
DB	2339	CTCCAAGCAGCCACAAAGATGAGGAGGAGTCACTTCCAGGAATTTATGATCTCTGT	2398
QY	1740	TTGATATGAAAGCAAAAGTGAACCTTCCAAAGGCTTGGGAGATGTGAAGAGACGATTT	1799
DB	2399	TTGATATGAAAGCAAAAGTGAACCTTCCAAAGGCTTGGGAGATGTGAAGAGACGATTT	2458
QY	1800	CTGTTGACAGCTTCACAGTGCAGAGCAGCTGCAGAGACTTTGAGTAAGAGG	1859
DB	2459	ATGTTGACAGCTTCACAGTGCAGAGCAGCTGCAGAGACTTTGAGTAAGAGG	2518
QY	1860	ATTCCTTGAAGACCTCTGATGATGATTTGTGTGATGTCATCTC--AAAGATTAATG	1917
DB	2519	ATTCCTTGAAGACCTCTGATGATGATTTGTGTGATGTCATCTC--AAAGATTAATG	2578
QY	1918	GTAATATGATAAATTTTAAATTTGATATTTGAATTAAGTGAATTTTAAATTA	1977
DB	2579	GTAATATGATAAATTTTAAATTTGATATTTGAATTAAGTGAATTTTAAATTA	2638
QY	1978	AAAAAAAAAAAAAAAA 1992	
DB	2639	AAAAAAAAAAAAAAAA 2653	

RESULT 5
HUMPSM 2653 bp mRNA linear PRI 08-JAN-1995
LOCUS Human prostate-specific membrane antigen (PSM) mRNA, complete cds.

QY	1020	TGCTATCAACCTACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAAGGCAATCTC	1079
DB	1679	TGGACACAACTACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAAGGCAATCTC	1738
QY	1080	TTTATGAAGTGGACATAAAAAGCTCTCCAGAGTTCAGAGGATGGCCAGGATTA	1139
DB	1739	TTTATGAAGTGGACATAAAAAGCTCTCCAGAGTTCAGAGGATGGCCAGGATTA	1798
QY	1140	GCAAAATGGGATCGGAAATGATTTTGGAGTGTCTTCCAAAGCATTGGAATTCCTCAG	1199
DB	1799	GCAAAATGGGATCGGAAATGATTTTGGAGTGTCTTCCAAAGCATTGGAATTCCTCAG	1858
QY	1200	GCAGAGCAGGTATACATAAAATTTGGGAACAAACAAATTCAGGGCTATCCATGATTC	1259
DB	1859	GCAGAGCAGGTATACATAAAATTTGGGAACAAACAAATTCAGGGCTATCCATGATTC	1918
QY	1260	ACAGTGTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	1319
DB	1919	ACAGTGTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	1978
QY	1320	ACCTCACTGTGGCCAGGTTTCGAGAGGAGATGTGTTTGGCTAGCCAAATTCATAGTGC	1379
DB	1979	ACCTCACTGTGGCCAGGTTTCGAGAGGAGATGTGTTTGGCTAGCCAAATTCATAGTGC	2038
QY	1380	TCCCTTTGATGTGCGAGATTATCTGATGTTTAAAGAAATGATGCGACAAATCTACA	1439
DB	2039	TCCCTTTGATGTGCGAGATTATCTGATGTTTAAAGAAATGATGCGACAAATCTACA	2098
QY	1440	ATATTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	1499
DB	2099	ATATTCTATGAACAAATGATGTTGGTGAAGTATTTATGATCCATGTTTAAATATC	2158
QY	1500	TTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAAAGTTCAGGAGAGCTCAGAGACT	1559
DB	2159	TTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAAAGTTCAGGAGAGCTCAGAGACT	2218
QY	1560	TTGCAAAAGCAACCCATATTTGTAAGAATGATGAATGATCACTCATGTTCTGGA	1619
DB	2219	TTGCAAAAGCAACCCATATTTGTAAGAATGATGAATGATCACTCATGTTCTGGA	2278
QY	1620	GAGCATTTATGATTCATTAGGTTTACAGACAGACCTTTTATAGCATGATCTATG	1679
DB	2279	GAGCATTTATGATTCATTAGGTTTACAGACAGACCTTTTATAGCATGATCTATG	2338
QY	1680	CTCCAAGCAGCCACAAAGATGAGGAGGAGTCACTTCCAGGAATTTATGATCTCTGT	1739
DB	2339	CTCCAAGCAGCCACAAAGATGAGGAGGAGTCACTTCCAGGAATTTATGATCTCTGT	2398
QY	1740	TTGATATGAAAGCAAAAGTGAACCTTCCAAAGGCTTGGGAGATGTGAAGAGACGATTT	1799
DB	2399	TTGATATGAAAGCAAAAGTGAACCTTCCAAAGGCTTGGGAGATGTGAAGAGACGATTT	2458
QY	1800	CTGTTGACAGCTTCACAGTGCAGAGCAGCTGCAGAGACTTTGAGTAAGAGG	1859
DB	2459	ATGTTGACAGCTTCACAGTGCAGAGCAGCTGCAGAGACTTTGAGTAAGAGG	2518
QY	1860	ATTCCTTGAAGACCTCTGATGATGATTTGTGTGATGTCATCTC--AAAGATTAATG	1917
DB	2519	ATTCCTTGAAGACCTCTGATGATGATTTGTGTGATGTCATCTC--AAAGATTAATG	2578
QY	1918	GTAATATGATAAATTTTAAATTTGATATTTGAATTAAGTGAATTTTAAATTA	1977
DB	2579	GTAATATGATAAATTTTAAATTTGATATTTGAATTAAGTGAATTTTAAATTA	2638
QY	1978	AAAAAAAAAAAAAAAA 1992	
DB	2639	AAAAAAAAAAAAAAAA 2653	

RESULT 5
HUMPSM 2653 bp mRNA linear PRI 08-JAN-1995
LOCUS Human prostate-specific membrane antigen (PSM) mRNA, complete cds.

QY 480 CTTTCATCCAGTTGGATCTATGATGCACAGAGCTCCTAGAAAAATGGTGGCTCAG 539
|||||
Db 1139 CTGTTTCATCCAAATTGGATCTATGATGCACAGAGCTCCTAGAAAAATGGTGGCTCAG 1198
QY 540 CACCCACAGATAGCAGCTGGAGAGAGAGTCTCAAAAGTGTCTCAAAATGTTTGAACCTGGCT 599
|||||
Db 1199 CACCCACAGATAGCAGCTGGAGAGAGAGTCTCAAAAGTGTCTCAAAATGTTTGAACCTGGCT 1258
QY 600 TTACTGGAAACTTTCTACAAAAAGTCAAGATGACATCCACTCTACCAATGAAAGTGA 659
|||||
Db 1259 TTACTGGAAACTTTCTACAAAAAGTCAAGATGACATCCACTCTACCAATGAAAGTGA 1318
QY 660 CGAGATTTTCAATGTGATAGTACTCTCAGAGAGAGCAGTGGAAACAGACAGATATGTCA 719,
|
Db 1319 CAAGATTTTCAATGTGATAGTACTCTCAGAGAGAGCAGTGGAAACAGACAGATATGTCA 1378
QY 720 TTCTGGAGAGTCAACGGGAGCTCATGGGTGTTTGTGTGTAATTGAACCTCAGAGTGAAGCAG 779
|||||
Db 1379 TTCTGGAGAGTCAACGGGAGCTCATGGGTGTTTGTGTGTAATTGAACCTCAGAGTGAAGCAG 1438
QY 780 CTGTTGTTCAGAACTGTGAGAGAGCTTGSAACTGTGAAAAAGAAAGGTTGAGACCTTA 839
|||||
Db 1439 CTGTTGTTCAGAACTGTGAGAGAGCTTGSAACTGTGAAAAAGAAAGGTTGAGACCTTA 1498
QY 840 GAAGAACAAATTTGTTTGCAGAGCTGGGATGCAGAGAAATTTGCTCTTGGTGTCTACTG 899
|||||
Db 1499 GAAGAACAAATTTGTTTGCAGAGCTGGGATGCAGAGAAATTTGCTCTTGGTGTCTACTG 1558
QY 900 AATGGGACAGAGATTAATTCAGACATCTTCAGAGCGTGGCTGCTTATTTATGCTG 959
|||||
Db 1559 AATGGGACAGAGATTAATTCAGACATCTTCAGAGCGTGGCTGCTTATTTAAATGCTG 1618
QY 960 ACTCATCTATAGAGAACTACACTGTGAGAGTGTATGTATACACAGATGATACAGCT 1019
|||||
Db 1619 ACTCATCTATAGAGAACTACACTGTGAGAGTGTATGTATACACAGATGATACAGCT 1678
QY 1020 TGGTATACAACTTAACAAAGAGCTGAAAAAGCCGTGATGAAGCTTTTGAAGCAATCTC 1079
|||||
Db 1679 TGGTATACAACTTAACAAAGAGCTGAAAAAGCCGTGATGAAGCTTTTGAAGCAATCTC 1738
QY 1080 TTTATGAAGTTGGACTAAAAAAATCCTCTCCCAAGAGTTCAAGTGGCATGCCAGATTA 1139
|||||
Db 1739 TTTATGAAGTTGGACTAAAAAAATCCTCTCCCAAGAGTTCAAGTGGCATGCCAGATTA 1798
QY 1140 GCAAAATTTGGGATCTGAGAAATGATTTTGGAGTGTCTTCCAGAGCTTGGAAATTTGCTCAG 1199
|||||
Db 1799 GCAAAATTTGGGATCTGAGAAATGATTTTGGAGTGTCTTCCAGAGCTTGGAAATTTGCTCAG 1858
QY 1200 GCAGAGCAAGGTATCTAAAAAATTTGGGAAACAAACAAATTCAGCGCTATCCACTGTATC 1259
|||||
Db 1859 GCAGAGCAAGGTATCTAAAAAATTTGGGAAACAAACAAATTCAGCGCTATCCACTGTATC 1918
QY 1260 ACAGTGTCTATGAAACATATGAGTGTGTGGAAAAAGTTTATGATCCCATGTTTAAATATC 1319
|||||
Db 1919 ACAGTGTCTATGAAACATATGAGTGTGTGGAAAAAGTTTATGATCCCATGTTTAAATATC 1978
QY 1320 ACCCTACTGTGGCCAGGTTTGGAGAGAGGATGTGTGTTGAGTACCAATTCATATAGTGC 1379
|||||
Db 1979 ACCCTACTGTGGCCAGGTTTGGAGAGAGGATGTGTGTTGAGTACCAATTCATATAGTGC 2038
QY 1380 TCCCTTTTGGATTTGAGATTAATGCTGTAGTTTAAAGAAAGTATGCTGCAAAATCTTCA 1439
|||||
Db 2039 TCCCTTTTGGATTTGAGATTAATGCTGTAGTTTAAAGAAAGTATGCTGCAAAATCTTCA 2098
QY 1440 ATATTTCTATGAAACATCCACAGGAAATGAGACATATACAGTTTATCATTTTGTACTTT 1499
|||||
Db 2099 GTATTTCTATGAAACATCCACAGGAAATGAGACATATACAGTTTATCATTTTGTACTTT 2158
QY 1500 TTTCTGCAAGTAAAAAATTTTACAGAAATTTGCTTCCAAAGTTCAGAGAGACATCCAGGACT 1559
|||||
Db 2159 TTTCTGCAAGTAAAAAATTTTACAGAAATTTGCTTCCAAAGTTCAGAGAGACATCCAGGACT 2218

QY 1560 TTGACAAAAGCAACCCAAATATTGTTAAGATGATGAATGATCACTATGTTTGGAAA 1619
|||||
Db 2219 TTGACAAAAGCAACCCAAATATTGTTAAGATGATGAATGATCACTATGTTTGGAAA 2278
QY 1620 GAGCATTTTATGATTCATTAGGTTTACACAGACAGACCTTTTATATAGCATGTCTATG 1679
|||||
Db 2279 GAGCATTTTATGATTCATTAGGTTTACACAGACAGACCTTTTATATAGCATGTCTATG 2338
QY 1680 CTCGAAAGCCGCAACAAAGTATGCAAGGGGAGCTCAATCCAGGAATTTATGATGCTCTGT 1739
|||||
Db 2339 CTCGAAAGCCGCAACAAAGTATGCAAGGGGAGCTCAATCCAGGAATTTATGATGCTCTGT 2398
QY 1740 TTGATATTGAAAGCAAAAGTGAAGCCCTTCCAAAGCCCTGGGAGATGTGAAGACAGATT 1799
2399 TTGATATTGAAAGCAAAAGTGAAGCCCTTCCAAAGCCCTGGGAGATGTGAAGACAGATT 2458
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Db 2639 AAAAAAAAAAAAAA 2653

RESULT 6
AF176574
LOCUS 2518 bp mRNA linear PRI NOV-2000
DEFINITION Homo sapiens folylpoly-gamma-glutamate carboxypeptidase (FGCP)
ACCESSION AF176574
VERSION complete cds.
KEYWORDS AF176574.1 GI:5762481
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2518)
Devlin,A.M., Ling,E.H., Pearson,J.M., Fernando,S., Clarke,R.,
Smith,A.D. and Halsted,C.H.
Glutamate carboxypeptidase II: a polymorphism associated with lower
levels of serum folate and hyperhomocysteinemia
Hum. Mol. Genet. 9 (19), 2837-2844 (2000)
PUBMED 11092759
REFERENCE 2 (bases 1 to 2518)
Devlin,A.M., Ling,E.-H. and Halsted,C.H.
Direct Submision
Submitted (09-AUG-1999) Internal Medicine, University of
California, Davis, TB 156, Davis, CA 95616, USA
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Matches 1717;	Conservative 0;	Mismatches 24;	Indels 2;	Gaps 1;
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Db	776	AGGTTAAATGCGCAGCTGCGAGGCGCAAGAGCATCTCTACTCAGACCCCTGCTG	835	
Db	300	ACTACTTGTCTCTGGGGTGAAGTCTCTACAGAGGTTGGAATCTTCTGGAGGTG	359	
Db	836	ACTACTTGTCTCTGGGGTGAAGTCTCTACAGAGGTTGGAATCTTCTGGAGGTG	895	
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Db	1016	CTGTTTCATCCAGTTGGATGATGATGACAGAGAGCTCTTGAAGAAATGGGTGCTG	1075	
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Db	1676	GCAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAAAGCATCTTGAATGCTTCAAG	1735	
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Db	1736	GCAAGAGACGATTAATTAATTAATTTGGGAAACAAATTCAGGCGCTATCCATGATTC	1795	
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Db	1916	TCCCTTTGATTTGTCAGATTTATCTGATTTTAAAGATATGTCGACAAAATCTACA	1975	
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Db	1976	ATATTTCTATGAACATATGATGTTGGAAGATGATGATGATGATGATGATGATGATG	2035	
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Db	2456	GTAATATTAATTAATTTTAAATTTGGTATATTTGAATTAATTTGAATTAATTAATTA	2515	
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Db	2516	AAA 2518		

RESULT 7
 AX376036
 LOCUS
 DEFINITION Sequence 103 from Patent WO0168848.
 ACCESSION AX376036

VERSION	AX376036.1	GI:19170410
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	1 Baker, K.P., Chen, J., Desnovers, L., Godard, A., Godowski, P.J., Gunney, A.L., Pan, J., Smith, V., Matanabe, C.K., Wood, W.I. and Zhang, Z.	
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same	
JOURNAL	Patent: WO 0168848-A 103 20-SEP-2001;	
FEATURES	Genentech, Inc. (US)	
source	Location/Qualifiers	
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Best Local Similarity	98.6%;	Pred. No. 0;
Matches 1713;	Conservative 0;	Mismatches 23; Indels 2; Gaps 1;
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AX467227			
LOCUS			
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DEFINITION	Sequence 1 from Patent WO0234287.
ACCESSION	AA467227
VERSION	AA467227.1 GI:21900509
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	1 Beier, A.M., Gautam, A. and Mouritsen, S.R. Novel therapeutic vaccine formulations Patent: WO 0234287-A 1 02-MAY-2002; Pharmexa A/S (DK)
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OY	300 ACTACTTGCCTCCGGGGTGAAGTCCCTATCCAGAGGTTGGAATCTCCTGGAGGTGGG 359
DB	698 ACTACTTGCCTCCGGGGTGAAGTCCCTATCCAGAGGTTGGAATCTCCTGGAGGTGGG 757
OY	360 TCCACGCTGGAATATCCCTAAATCGAATGTGCGAGAGACCTCTCACACAGGTTACC 419
DB	758 TCCACGCTGGAATATCCCTAAATCGAATGTGCGAGAGACCTCTCACACAGGTTACC 817
OY	420 CAGCAATGATATCGCTTATAGCATGGATGGATGCGAGAGGCTGTGGCTTCCAGTATTC 479
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DB	938 CACCAACAGATGACGCTGGAGAGAGAAGCTCAAGATGCTCTACACATGTTGAGCTGGCT 997
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QY	720	TTTCGCGAGGCTACCCGGGACTCATGGGGTGTGGTGAATTTGACCTCAGAGTGGACAG	779
Db	1118	TTTCGCGAGGCTACCCGGGACTCATGGGGTGTGGTGAATTTGACCTCAGAGTGGACAG	1177
QY	780	CTGTGTTTCATGAAGAACTGTGAGAGCTTTGGAAACCTGAAAAAGAGGGGTGAGACTTA	839
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Db	1238	GAAGAAACAAATTTGTTTGCAGAGCTGGAGTGCAGAAATTTGGTCTTCTTGCTTCTACTG	1297
QY	900	AGTGGGCGAGAGATATTTCAAGACTCCTTCAAGAGCGTGGGTGGCTATATTAAATCTG	959
Db	1298	AGTGGGCGAGAGAGATTTCAAGACTCCTTCAAGAGCGTGGGTGGCTATATTAAATCTG	1357
QY	960	ACTACTATATGAAGAAACTACACTCGAAGATTGATTGACACCACTGATGTACAGCT	1019
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QY	1440	ATATTTCTATGAACATCCACAGGAAATGABAGACATACAGTTTATCATTTGATTCACATT	1499
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QY	1500	TTTTCGAGTAAAAAATTTACAGAAATTTGCTCCAGTCCAGTCAGCAGAGACTCCAGACT	1559
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RESULT 9
AY101595 2253 bp mRNA linear PRI 27-MAY-2002
LOCUS Homo sapiens prostate-specific membrane antigen mRNA, complete cds.
DEFINITION
ACCESSION AY101595
VERSION AY101595.1 GI:21217742
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 2253)
TITLE Ye,C.Z., Zhang,F.L., Zhang,Y.K. and Chen,C.Q.
Cloning and sequencing of Chinese prostate-specific membrane
antigen
JOURNAL MianYuxue Zazhi 17 (5), 328-330 (2001)
REFERENCE 2 (bases 1 to 2253)
AUTHORS Ye,C.Z.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002), Department of Urology, Zhongshan Hospital,
Medical Center of Fudan University, Fenglin Rd 180, Shanghai
200032, China

FEATURES
source Location/Qualifiers
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/country="China"
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LAGAGVILTSDDADYAPAGVKSYPGQMN.PGGVORGNILNINAGADPLTPPYANE
YATRGIAEAVGLPSTFVPIHIGYTDQKLEKKGSGAPPSMRGSLKXYVNGPQT
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AAAEITLSEVA"

BASE COUNT 670 a 449 c 527 g 607 t
ORIGIN

Query Match 79.4%; Score 1582.4; DB 9; Length 2253;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 240 AGGTTAAATAGCCAGCTGGAGGGCCAAAGAGCATTTCTACTCAGACCCCTG 299
Db 638 AGGTTAAATAGCCAGCTGGAGGGCCAAAGAGCATTTCTACTCAGACCCCTG 697
Qy 300 ACTACTTGTCTCTGGGGTGAAGTCTATCCAGAGCGTTGGAATCTTCTGAGAGTGTG 359

Db 698 ACTACTTGTCTCTGGGGTGAAGTCTATCCATCAGATGTTGGAATCTTCCGAGAGTGTG 757
Qy 360 TCCAGCGTGAATATTCCTAAATCTGAATGCTGACAGACCTCTCACACCGAGTTAC 419
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Db 1238 GAAGAACAAATTTGTTGCAAGCTGGAGTGCAGAGAAATTTGTCCTTGGTCTACTG 1297
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Qy 1380 TCCCTTTGATGTGCGATTTATGCTGTAGTTTAAAGAAATGCTGACAAATCTACA 1439

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Qy 1500 TTTCTGCAAGTAAATAATTTTACAGAAATGCTTCCAGTTCAGCAGAGACTCCAGAGCT 1559
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Qy 1560 TTGACAAAAGCAACCCCATATTTGTAAAGATATGATATCATCTATGTTTCGGAAA 1619
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Qy 1620 GAGCATTTATGATTCATTAGAGGTATACAGACAGACCTTTTATAGCATGTCTATG 1679
Db 2018 GAGCATTTATGATTCATTAGAGGTATACAGACAGACCTTTTATAGCATGTCTATG 2077
Qy 1680 CTCACAGAGCCACACAAAGATATGAGGGAGTCAATCCAGAAATTTATGATGCTCTGT 1739
Db 2078 CTCACAGAGCCACACAAAGATATGAGGGAGTCAATCCAGAAATTTATGATGCTCTGT 2137
Qy 1740 TTGATATGAAAGCAAGATGAGAGGAGTCAATCCAGAAATTTATGATGCTCTGT 1799
Db 2138 TTGATATGAAAGCAAGATGAGAGGAGTCAATCCAGAAATTTATGATGCTCTGT 2197
Qy 1800 CTGTTGACAGCCTTTCACAGTGCAGGAGCTGCAGAGACTTTGAGTACAGAGCTTAA 1855
Db 2198 ATGTTGACAGCCTTTCACAGTGCAGGAGCTGCAGAGACTTTGAGTACAGAGCTTAA 2253

RESULT 10
LOCUS BC025672 2472 bp mRNA linear PRI 11-MAR-2002
DEFINITION Homo sapiens, similar to folate hydrolase (prostate-specific membrane antigen) 1, clone MGC:34488 IMAGE:5202715, mRNA, complete cds

ACCESSION BC025672
VERSION BC025672.1 GI:19343603
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2472)
Straussberg, R.
Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland:
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastello, C., Mastian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantirip, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

REMARK
COMMENT
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAX Plate: 49 Row: e Column: 5

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LAGKGVLTGSDPADYFAPGVKSYPDGNNLPGGGORNNLILNAGDPLNPGYANE
YARRGIAEAVGLSEIPIPHYIGYDAOKLLEKMGSSAPPSDSRLKVPYNGPRT
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DPMFEYHLITVAOVGRWFEELANSIVLEPDCRDAAVYLRKADKIYSISMHPDMKT
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BASE COUNT 746 a 483 c 594 g 649 t
ORIGIN

Query Match 75.9%; Score 1511.4; DB 9; Length 2472;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 1639; Conservative 0; Mismatches 21; Indels 95; Gaps 2;

Qy 240 AGGTTAAAGTCCAGCTGGCAGGGGCCAAAGAGTCTTCTACTACAGACCTGCTG 299
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Qy 300 ACTACTTTGCTCTCTGGGTGAAGTCTTATCCAGACGTTTGAATTTCTCTGAGGTGGT 359
Db 857 ACTACTTTGCTCTCTGGGTGAAGTCTTATCCAGATGTTGAATTTCTCTGAGGTGGT 916
Qy 360 TCCACGCTGGAATATCTTAATCTGAATGGGAGGAGACCTCTCACACAGGTTACC 419
Db 917 TCCACGCTGGAATATCTTAATCTGAATGGGAGGAGACCTCTCACACAGGTTACC 976
Qy 420 CAGCAATGAATACGCTTATAGGATGAGATTTGACAGAGCTGTTGGTCTCCAACTATTC 479
Db 977 CAGCAATGAATATACGCTTATAGGATGAGATTTGACAGAGCTGTTGGTCTCCAACTATTC 1036
Qy 480 CTGTTTCATCCAGTTGGATATGATGATGACAGAGACCTCTAGAAAAATTTGGTGGCTAG 539
Db 1037 CTGTTTCATCCAGTTGGATATGATGATGACAGAGACCTCTAGAAAAATTTGGTGGCTAG 1096
Qy 540 CACACACAGATAGCAGCTGAGAGAGATCTCAAGAGTCTCTACATGTTGGACCTGGCT 599
Db 1097 CACACACAGATAGCAGCTGAGAGAGATCTCAAGAGTCTCTACATGTTGGACCTGGCT 1156
Qy 600 TTACTGGAACCTTTTCTACAAAAAGTCAAGATGCACATCCATCTACCAATGAATGA 659
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Qy 720 TTCTGGAGAGTCACCGGAGCTCATGGGTTTGGGTGATTTGACCTCAGAGTGGAGCAG 779
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QY	420	CAGCAAAATGAAATACGCTTATAGGCATGGAATTCGAGAGGCGTGTGCTTCACATGATATC	479
Db	967	CAGCAAAATGAAATAGCGCTTACGACTTCAAATCGAGAGGCGTGTGCTTCACAGATATC	1026
QY	480	CTGTTCATCCAGTTGGATCTATGATGACAGAAAGCTCTAGAAAAAATGGGTGGCTCAG	539
Db	1027	CTGTTCATCCAGTTGGATCTCTGATGACAGAGAGCTCTTGAAAAAATGGGTGGATCCG	1086
QY	540	CACCAACCAATAGAGCTGGAGAGAGTCTCAAAGTGTCTTAATGTTGGACTGTGCT	599
Db	1087	CACCCCAAGATGACAGTTGGAAAGAAAGTCCACAGTCCCTTAACAATGTGGTCTGTGTT	1146
QY	600	TTACTGGAACTTTCTACAAAAAGTCAGATGTCACATCCACTCTTACCAATGAGTGA	659
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QY	840	GAAGAACAAATTTGTTTGGCAAGCTGGAGTGCAGAAATTTGGTCTTCTTGTTGTTCTACTG	899
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QY	1020	TGATATACAACTTAACAAAAGAGCTGAAAGCCCTGATGAAAGCTTTGAAAGCAAAATCTC	1079
Db	1567	TGATATACAACTTAACAAAAGAGCTGCCAAGTCTGATGAAAGGTTTGAAGGCAAAATCTC	1626
QY	1080	TTTATGAAAGTTGGACTTAATAAAAGTCTTCCAGAGTTGATGTCAGTCCCAAGATTA	1139
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QY	1140	GCAAAATTTGGGTGCGAAATGATTTTGGAGTGTCTTCCAAAGCACTTGGAAATGCTCTCAG	1199
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QY	1260	ACAGTGTCTATGAAACATATGAGTGTGGTGGAAAAGTTTATGATCCAAATGTTTAATATATC	1319
Db	1807	ACAGTGTCTATGAAACATATGAAATTTAGTGGAAAAGTTTATGACCCAACTTTTAAAGTATC	1866
QY	1320	ACCCACATGAGGCGGAGGTTTCGAGAGAGAGTGGTGTGAGCTGACCAATTCCTATATGAC	1379
Db	1867	ATCTTGCTGTGCGCCAGGTTTCGAGAGAGAAATTTGTTTCGAACTTGGCCAAATTCGTATGTC	1926
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Db	1927	GCCCTTTTGATGTCGAGATATATGCTGTAGTTTAAAGAAATTTAGTGTGATTAACCTTACA	1986
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QY	1560	TTGCACAAAGCACCCCATATTGTTAAGATGATGAATGATCAACTATCTTTCTGCAAA	1619
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QY	1620	GAGATTTATTTGATCTTTTGGGGTTTACGACGACACCTTTTATAGGCATGCTATCATG	1679
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QY	1680	CTCCACACGACGCACACAAAGATGATCAGGAGGAGTATTTCCACAGAAATTTATGATGCTGTG	1739
Db	2227	CTCCACAGCAGCCACACAAAGATGATGAGGAGGAGTATTTCCACAGGATGATGATGAGCTGTG	2286
QY	1740	TTGATATTGAAGAAGAGTGGACCCCTTCCAAAGGCTTGGGAGAGATGTGAAGACACAGATTT	1799
Db	2287	TTGATATTGAAGAAGAGTGGAGTGGATCTTCCAAAGGCTTGGGAGAGATGTGAAGACAGATTT	2346
QY	1800	CTGTGTGACGCTTACAGTGCAGGACGACTGTGAGAGACTTTGTAGTACGAGTGGCCATAAG	1859
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QY	1920	ATATTGATTAATTTTAAATTTGTAATTTTGAATTAAGTTGAATTTATATATATAAAAA	1979
Db	2467	GTATTGATTAATCTGAATAATTAAGTGTGTGATCATATGATATCATATGTAGAGATAAAAA	2526
QY	1980	AAAAAA 1985	
Db	2527	AAAAAA 2532	

RESULT 13

LOCUS	RNU75973	2899 bp	mRNA	linear	ROD 05-NOV-1997
DEFINITION	Rattus norvegicus NAAG-peptidase mRNA, complete cds.				
ACCESSION	U75973				
VERSION	U75973.1 GI:1661226				
KEYWORDS					
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (bases 1 to 2899)				
AUTHORS	Bzdega,T., Turi,T., Wroblewska,B., She,D., Chung,H.S., Kim,H. and				
	Neale,J.H.				
TITLE	Molecular cloning of a peptidase against N-acetylaspartylglutamate				
JOURNAL	from a rat hippocampal cDNA library				
MEDLINE	J. Neurochem. 69 (6), 2270-2277 (1997)				
PUBMED	98041505				
REFERENCE	2 (bases 1 to 2899)				
AUTHORS	Bzdega,T., Turi,T., Wroblewska,B., She,D. and Neale,J.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-OCT-1996) Biology, Georgetown University, 37th & O				
	St. NW, Washington, DC 20057, USA				
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Db	2402 AACAAAGTATAA_2413
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LOCUS AF040256	2348 bp mRNA linear ROD 24-MAR-1998
DEFINITION Rattus norvegicus glutamate carboxypeptidase II mRNA, complete cds	
ACCESSION AF040256	
VERSION AF040256.1 GI:2982228	
KEYWORDS	
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2348)	Luthi-Carter, R., Berger, U.V., Barczak, A.K., Enna, M. and Coyle, J.T. Isolation and expression of a rat brain cDNA encoding glutamate carboxypeptidase II Proc. Natl. Acad. Sci. U.S.A. 95 (6), 3215-3220 (1998)
JOURNAL MEDLINE	98169524
PUBMED	9501243
REFERENCE 2 (bases 1 to 2348)	Luthi-Carter, R., Berger, U.V., Barczak, A.K., Enna, M. and Coyle, J.T. Direct Submission Submitted (30-DEC-1997) Laboratory of Molecular and Developmental Neuroscience, Massachusetts General Hospital-East, Bldg. 149, 13th St., Rm. 2510, Charlestown, MA 02129, USA
AUTHORS JOURNAL	Location/Qualifiers
FEATURES	1..2348
SOURCE	/organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /tissue.type="brain" 72..2330 /EC.number="3.4.17.21" /note-"N-acetylated alpha-linked acidic dipeptidase (NAALadase); NAAG peptidase; similar to Homo sapiens prostate-specific membrane antigen (PSMA)" /codon_start=1 /product="glutamate carboxypeptidase II" /protein_id="AAC40067.1" /db_xref="GI:2982229" /translation="MMNAQODSDSAEALGRORFCACTIVLAFTGTFIIGFLGFMP KPSDSTSVSYPEMKKAFLDELKAENIKFVLNTRPHLAGOHNELAKOJHQAOK KEFDLDELVDLSYPKTKTPNYISITNEGNEIFKSILAEISPGVENISDVV PPYAFSPGCPEDGDIVYNARTREDPFKLRYWKINKSGKIYIARYQVRGNKKYK AOLGARGLITSDPADIFYFGVASIDYPAKMLPEGGVORAVNLNGADPLTGYPRI NEVAIRHEFEVALPSTIPVPIIDYDAOKLLEHGMSGAPDSMSKGGLKVAYWGP FAGNSQKVKRLHIHSYNKYRIYNVIGTLGAVEPDYVILGGHRDMVGADIPDOS GAAVHEIVRTGFKKKGMRRPTILEASDADEEGILGSTEMAEEHSRLROERGVA YGNDSIEGNTLRVDCOTPLMHSLVNLTLELPSPDGSEFGSKSLYDSMKRPSSTE IGMRISIKSGNDPEVFEOFLGASGARATRKMNKNKYSPLYHSYETTELVEVE FYDPTEFHLLTVAOYRGAMFELANSIYLPRDCOSYAALKKHETTINYISNMHPQE KAVNISDFSSFAVNFTDASKFNQRLODKSNPILRLINDQLMLERAFIDPLIC LPGPYFRHLITYAPSSHNKYAGESFPGLYDALFDLINNKVDTSKAMREYKRQISIAAF VOAAEFLREVD"
CDS	
BASE COUNT	706 a 484 c 537 g 621 t
ORIGIN	
Query Match	63.1%; Score 1257.2; DB 10; Length 2348;
Best Local Similarity	85.7%; Pred. No. 2.2e-277;
Matches 1397; Conservative	0; Mismatches 233; Indels 0; Gaps 0;
Dd	240 AGGTAAAAATGCCCAGCTGCAGGCGCCAAAGAAGTAGTATTCTGACTACAACCTGCTG 299
Oy	
Dd	715 AGGTTAAAATAGCTACGCTGCAGGTGCAAAAGAGATCATTCGTACACAGACCCTGCTG 774
Oy	
Dd	300 ACTACTTTGGCTCCGGGGTGAAGTCCATTCACAGAGGTGGAAATCTCTGAGGATGGTG 359
Oy	
Dd	775 ATTACTTTGTTCTCGGGGTGAAGTCTCTATCCAGATGTTGGAAACCTCCCTGAGAGTGGT 834
Oy	
Dd	360 TCCAGCGTGAATAATATCCTAATATCTGATGTGTGACAGGAACCTCTCACACAGGTTACC 419
Oy	

[illegible]

[illegible]

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; CLONE: Prostate-Specific Membrane Antigen
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 262..2511
; US-08-325-553-1

Query Match      85.5%; Score 1702.6; DB 1; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

OY      240 AGGTTAAATGCGCCAGCTGGGCGGCGCAAGAGGATCTCTCTACTCAGACCTCTG 299
      |||
      899 AGGTTAAATGCGCCAGCTGGGCGGCGCAAGAGGATCTCTCTACTCAGACCTCTG 958
      |||
OY      300 ACTACTTGGCTCCTGGGGTGAAGTCTATCCAGAGGTTGGAAATCTTCTGGAGGTG 359
      |||
      959 ACTACTTGGCTCCTGGGGTGAAGTCTATCCAGATGGTTGGAAATCTTCTGGAGGTG 1018
      |||
OY      360 TCCAGCGTGAATATCTCTAATCTGATGTGCGAGAGACCTCTCAGACAGGTTACC 419
      |||
      1019 TCCAGCGTGAATATCTCTAATCTGATGTGCGAGAGACCTCTCAGACAGGTTACC 1078
      |||
OY      420 CAGCAATGAAATACGCTTATFAGGATGAAATTCAGAGGCTGTGGTCTTCCAGTATTC 479
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      1079 CAGCAATGAAATACGCTTATFAGGATGAAATTCAGAGGCTGTGGTCTTCCAGTATTC 1138
      |||
OY      480 CTGTTTCATCCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 539
      |||
      1139 CTGTTTCATCCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1198
      |||
OY      540 CACCAACAGATAGAGCTGGAGAGAGAGTCTCAAGTCTCTCAAGTCTCTGAGACCTG 599
      |||
      1199 CACCAACAGATAGAGCTGGAGAGAGAGTCTCAAGTCTCTCAAGTCTCTGAGACCTG 1258
      |||
OY      600 TTACTGGAATCTTTCTACACAAAAGTCAAGATGACATCCACTCTACCAATGAATGA 659
      |||
      1259 TTACTGGAATCTTTCTACACAAAAGTCAAGATGACATCCACTCTACCAATGAATGA 1318
      |||
OY      660 CGAGAATTTACATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 719
      |||
      1319 CGAGAATTTACATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1378
      |||
OY      720 TTCTGGAGGTCACCGGACCTCATGGGTTGGTGGTATGACCTCAGAGTGGAGAG 779
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      1379 TTCTGGAGGTCACCGGACCTCATGGGTTGGTGGTATGACCTCAGAGTGGAGAG 1438
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OY      780 CTGTTGTCATGAAATCTGTGAGAGCTTTGGAAACACTGAAAAAGAGAGGTGGAGACCTA 839
      |||
      1439 CTGTTGTCATGAAATCTGTGAGAGCTTTGGAAACACTGAAAAAGAGAGGTGGAGACCTA 1498
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OY      840 GAAGAACATTTTGTTCGAAAGCTGGGATGCGAAGAAATTTGGTCTTCTGGTCTACTG 899
      |||
      1499 GAAGAACATTTTGTTCGAAAGCTGGGATGCGAAGAAATTTGGTCTTCTGGTCTACTG 1558
      |||
OY      900 AGTGGGAGAGGATATTCAGAGCTCTTCAAGAGCTGGGCTGATATATATATATGCTG 959
      |||
      1559 AGTGGGAGAGGATATTCAGAGCTCTTCAAGAGCTGGGCTGATATATATATATGCTG 1618
      |||
OY      960 ACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTTGATACACACTGATGTACAGCT 1019
      |||
      1619 ACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTTGATACACACTGATGTACAGCT 1678
      |||
OY      1020 TGGTATACACCTAACAAAAGAGCTGAAAAGCCCTGATGAGAGGCTTTGAAGCAATCTC 1079
      |||
      1679 TGGTATACACCTAACAAAAGAGCTGAAAAGCCCTGATGAGAGGCTTTGAAGCAATCTC 1738
      |||
OY      1080 TTTATGAAGTGGAGCTAAAAAGGCTCTCCAGAGTTCAGTGGCATGCCAGATTA 1139
      |||
      1739 TTTATGAAGTGGAGCTAAAAAGGCTCTCCAGAGTTCAGTGGCATGCCAGATTA 1798
      |||
OY      1140 GCAAAATGGGATCTGAAATGATTTTGAAGTGTCTTCCACAGACTTGGAAATGGTTCAG 1199
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      1799 GCAAAATGGGATCTGAAATGATTTTGAAGTGTCTTCCACAGACTTGGAAATGGTTCAG 1858
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OY      1200 GCAGAGCAGCGTATCTATAAAATTTGGAAACAAATTCAGGGCTATCTAGTATC 1259
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      1859 GCAGAGCAGCGTATCTATAAAATTTGGAAACAAATTCAGGGCTATCTAGTATC 1918
      |||
OY      1260 ACAGTGTCTATGAAACATATAGAGTGTGGAAAAAGTTTATGATCCAAATGTTAAATATC 1319
      |||
      1919 ACAGTGTCTATGAAACATATAGAGTGTGGAAAAAGTTTATGATCCAAATGTTAAATATC 1978
      |||
OY      1320 ACCTCACTGTGGCCAGGTTGAGAGAGGATGCTGTTTGAAGTACCAATTCATAGTGC 1379
      |||
      1979 ACCTCACTGTGGCCAGGTTGAGAGAGGATGCTGTTTGAAGTACCAATTCATAGTGC 2038
      |||
OY      1380 TCCCTTTGATGTGCGAGATTAATGCTAGTTTAAAGATATGCTGACAAATCTACA 1439
      |||
      2039 TCCCTTTGATGTGCGAGATTAATGCTAGTTTAAAGATATGCTGACAAATCTACA 2098
      |||
OY      1440 ATATTCTATGAACATTCACAGAGAAATGAAGCATACAGTTATCATTTGATTCATTT 1499
      |||
      2099 ATATTCTATGAACATTCACAGAGAAATGAAGCATACAGTTATCATTTGATTCATTT 2158
      |||
OY      1500 TTTCTGCAATGAAAAATTTTACAGAAATGCTTCCAAAGTTCAGCGAGAGACTCCAGACT 1559
      |||
      2159 TTTCTGCAATGAAAAATTTTACAGAAATGCTTCCAAAGTTCAGCGAGAGACTCCAGACT 2218
      |||
OY      1560 TTGCAAAAGCAACCAATATTTTAAAGATGATGAATGATCACTATGTTCTGGAAA 1619
      |||
      2219 TTGCAAAAGCAACCAATATTTTAAAGATGATGAATGATCACTATGTTCTGGAAA 2278
      |||
OY      1620 GAGCATTTATGATTCATTAAGGTTTACAGACAGACCTTTTATAGCATGTCTATG 1679
      |||
      2279 GAGCATTTATGATTCATTAAGGTTTACAGACAGACCTTTTATAGCATGTCTATG 2338
      |||
OY      1680 CTCCAAGCAGCCAAACAGATATCAGAGGAGTATCCCAAGAAATTTATGATGCTGT 1739
      |||
      2339 CTCCAAGCAGCCAAACAGATATCAGAGGAGTATCCCAAGAAATTTATGATGCTGT 2398
      |||
OY      1740 TTGATTTGAAAGCAAGTGGAGCTTCCAAAGCCTGGGAGATGTAAGAGACAGATTT 1799
      |||
      2399 TTGATTTGAAAGCAAGTGGAGCTTCCAAAGCCTGGGAGATGTAAGAGACAGATTT 2458
      |||
OY      1800 CTGTTGACGCTTACAGAGTGCAGGCTGAGAGCTTTGATGTAAGTGAAGCTTAAGAG 1859
      |||
      2459 ATGTTGACGCTTACAGAGTGCAGGCTGAGAGCTTTGATGTAAGTGAAGCTTAAGAG 2518
      |||
OY      1860 ATTCTTTAGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1917
      |||
      2519 ATTCTTTAGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2578
      |||
OY      1918 GTATATTGATTAATTTTAAATTTGATATTTGAATTAAGTGAATTTATATATATAA 1977
      |||
      2579 GTATATTGATTAATTTTAAATTTGATATTTGAATTAAGTGAATTTATATATATAA 2638
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OY      1978 AAAAAAAAAAAAAA 1992
      |||
      2639 AAAAAAAAAAAAAA 2653
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RESULT 2
US-08-394-152A-1
; Sequence 1, Application US/08394152A
; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
```

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STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-394-152A-1

Query Match      85.5%; Score 1702.6; DB 2; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
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QY 720 TTCTGGAGGTCACGGGACTCATGGGTGTTGGTGTATGACCTCAGAGTGGACAG 779
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Db 1379 TTCTGGAGGTCACGGGACTCATGGGTGTTGGTGTATGACCTCAGAGTGGACAG 1438
QY 780 CTGTGTGTCATGAACCTGTGAGAGCTTTGGAACTGAAAAAGGAGGTGAGACCTA 839
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Db 1439 CTGTGTGTCATGAACCTGTGAGAGCTTTGGAACTGAAAAAGGAGGTGAGACCTA 1498
QY 840 GAAGAACAAATTTTGTTCAGAGTGGGATGACAGAACAAATTTGTCTTCTTGGTCTACTG 899
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Db 1499 GAAGAACAAATTTTGTTCAGAGTGGGATGACAGAACAAATTTGTCTTCTTGGTCTACTG 1558
QY 900 AGTGGCAGAGATAATTCAGACTCTCCAGAGAGGTGGCGGCTTATTAATAGCTG 959
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Db 1559 AGTGGCAGAGAGAAATTAAGACTCTCCAGAGAGGTGGCGGCTTATTAATAGCTG 1618
QY 960 ACTCATCTATAGAAGAACTACACTGTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019
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Db 1619 ACTCATCTATAGAAGAACTACACTGTGAGAGTTGATTGTACACCACTGATGTACAGCT 1678
QY 1020 TGGTATACAACTTAACAAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAGCAATCTC 1079
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Db 1679 TGGTATACAACTTAACAAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAGCAATCTC 1738
QY 1080 TTTATGAAGTTGGACTAAAAAAGTCTCCCAAGTTTCAGTGGCATGCCAGGATPA 1139
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Db 1739 TTTATGAAGTTGGACTAAAAAAGTCTCCCAAGTTTCAGTGGCATGCCAGGATPA 1798
QY 1140 GCAAAATGGGATCTGGAATGATTTTGAGGTGTTCTCCAGAGCTTGGAAATGCTTCAG 1199
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Db 1799 GCAAAATGGGATCTGGAATGATTTTGAGGTGTTCTCCAGAGCTTGGAAATGCTTCAG 1858
QY 1200 GCAGAGCAGGTAATCTAAAAATTTGGGAAACAACAAATTCAGCGCTTATCCACTATC 1259
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Db 1859 GCAGAGCAGGTAATCTAAAAATTTGGGAAACAACAAATTCAGCGCTTATCCACTATC 1918
QY 1260 ACAGGTCTATGAACATATGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTAAATATC 1319
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Db 1919 ACAGGTCTATGAACATATGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTAAATATC 1978
QY 1320 ACCTCAGTGGGCCAGGTTTCGAGAGGAGTGTGTTGAGCTAGCCAAATTCATPAGTGC 1379
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Db 1979 ACCTCAGTGGGCCAGGTTTCGAGAGGAGTGTGTTGAGCTAGCCAAATTCATPAGTGC 2038
QY 1380 TCCCTTTGATGTGAGATTTATGCTGTAGTTTAAAGAAATGCTGACAAATCTACA 1439
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QY 1440 ATATTTCTATGAACATCCACAGGAATGAAGCATACAGTTTATCATTTGATTCCTTT 1499
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Db 2399 TTGATATTGAAGCAAAAGTGGACCTTCCAAAGGCTGGGGAAGTGAAGAGACAGATT 2458
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1860 ATTCTTTAGAGACTCTGTAATGTAATTTGCTGTAAGTACCTC - AAAGATATATATG 1917
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OY 2519 ATTCTTTAGAGAACTGATGTAATTTGCTGTAAGTACCTCAGAAAGATGCTAATG 2578
1918 GATATTTGATTAATTTTAAATTTGTAATTTGTAATTAAGTTGAATTTATATATATATA 1977
2579 GTATATTGATAATTTTAAATTTGTAATTTGTAATTAAGTTGAATTTATATATATA 2638
OY 1978 AAAAAAAAAAAAAA 1992
2639 AAAAAAAAAAAAAA 2653
RESULT 3
US-08-705-477E-1
; Sequence 1, Application US/08705477E
; Patent No. 6569432
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Plato, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-G
; CURRENT APPLICATION NUMBER: US/08/705,477E
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-705-477E-1
Query Match 85.5%; Score 1702.6; DB 4; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
OY 240 AGGTTAAATATGCCAGCTGCGAGGGGCCAAAGAGTCATCTCTACTCAGACCTGCTG 299
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Db 899 AGGTTAAATATGCCAGCTGCGAGGGGCCAAAGAGTCATCTCTACTCAGACCTGCTG 958
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|||||
Db 959 ACTACTTTGCTCCGCGGGTGAAGTCCATATCCAGAGGTTGAATCTTCTGAGGCTG 1018
360 TCCAGCGTGAATATCCTTAATCTGAATGTTGAGAGACCTCTCAGACAGGTTACC 419
1019 TCCAGCGTGAATATCCTTAATCTGAATGTTGAGAGACCTCTCAGACAGGTTACC 1078
OY 420 CAGCAAAATGAATACGCTTATAGGATGGAATTCAGAGGCTGTTGCTTCCAAATATTC 479
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1139 CTGTTTCATCCAGTTGGATACATATGATGCAGAGAAAGCTCCTAGAAAAATTTGGTGGCTAG 1198
OY 540 CACACACGATAGAGCTGAGAGAGAGTCCAAAGTGTCTACAAATTTGGAGCTGCT 599
1199 CACACACGATAGAGCTGAGAGAGAGTCCAAAGTGTCTACAAATTTGGAGCTGCT 1258
OY 600 TTACTGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAATGA 659
1259 TTACTGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAATGA 1318
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780 CTGTTTCATGAATTTGAGAGAGCTTTGGAACACTGAAAAAGAGGTTGAGACCTTA 839
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OY 840 GAAGAACAAATTTGTTTGCAGGATGCGAGAAATTTGCTCTTGTCTACTG 899
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OY 1080 TTTATGAAGTTGAGCTTAACAAAGCTCTTCCAGAGCTTCATGAGGATCCCAAGATA 1139
1739 TTTATGAAGTTGAGCTTAACAAAGCTCTTCCAGAGCTTCATGAGGATCCCAAGATA 1798
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OY 1260 ACACTGCTATGAACATATGAGTGTGGGAAAGTTTATGATTCGAATGTTAAATATC 1319
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OY 1320 ACCATCATGAGGCCAGGTTGAGAGAGAGTGTGTTGAGCTGACCAATTCATAGTC 1379
1979 ACCATCATGAGGCCAGGTTGAGAGAGAGTGTGTTGAGCTGACCAATTCATAGTC 2038
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2219 TTGAACAAAGCAACCAATATTTTGAAGATGATGATCAATCTATGTTCTGAAA 2278
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QY	1800	CTGTTGCAGCCTTACAGCTGCAGCAGCTGCAGAGACTTTGATGTAAGTACCTTAAGAGG	1859
Db	2459	ATGTTGACGCTTACAGCTGCAGCAGCTGCAGAGACTTTGATGTAAGTACCTTAAGAGG	2518
QY	1860	ATTCCTTGAACACCTGATGTAATTTGTGTGATGCTACTC--AAAGATTAATAAGG	1917
Db	2519	ATTCCTTGAAGAAATCCGATTGAATTTGTGTGTGCTCACTCGAAGAAATCGTAAGG	2578
QY	1918	GTATATTGATTAATTTTAAATTTGGTATATTTGAAATTAAGTTGAAATTTATATATAAA	1977
Db	2579	GTAATATTGATTAATTTTAAATTTGGTATATTTGAAATTAAGTTGAAATTTATATATAAA	2638
QY	1978	AAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAA 2653	
Result 4			
US-08-705-477E-100			
; Sequence 100, Application US/08/05477E			
; Patent No. 6569432			
; GENERAL INFORMATION:			
; APPLICANT: Israeli, Ron S			
; APPLICANT: Heston, Warren D.W.			
; APPLICANT: Fair, William R.			
; APPLICANT: Overfelli, Onathek			
; APPLICANT: Pinto, John			
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF			
; FILE REFERENCE: 1769/41426-G			
; CURRENT APPLICATION NUMBER: US/08/705,477E			
; NUMBER OF SEQ ID NOS: 128			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 100			
; LENGTH: 2387			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-08-705-477E-100			
Query Match			
Best Local Similarity 84.5%; Score 1683.4; DB 4; Length 2387;			
Matches 1717; Conservative 0; Mismatches 36; Indels 2; Gaps 1;			
QY	240	AGGTTAAATATGCCAGCTGCGAGGGGCCAAAGAGTCAATTCCTACTCAGACCCCTGCTG	299
Db	633	AGGTTAAATATGCCAGCTGCGAGGGGCCAAAGAGTCAATTCCTACTCAGACCCCTGCTG	692
QY	300	ACTACTTGGCTCGGGGGTGAAGTCCATCCAGAGGGTTGAATCTTCCTGGAGGTGGTG	359
Db	693	ACTACTTGGCTCGGGGGTGAAGTCCATCCAGAGGGTTGAATCTTCCTGGAGGTGGTG	752
QY	360	TCCAGCGTGAATATCCTAAATCTGAATGTGTGACGAGACCCCTCTCACACAGTTTACC	419
Db	753	TCCAGCGTGAATATCCTAAATCTGAATGTGTGACGAGACCCCTCTCACACAGTTTACC	812
QY	420	CAGCAAAATGATAGCCTTATAGCGATGGAATTGACAGAGCGCTTGTGTTCCAAAGTATTC	479
Db	813	CAGCAAAATGATAGCCTTATAGCGATGGAATTGACAGAGCGCTTGTGTTCCAAAGTATTC	872
QY	480	CTGTTCAATCAGTTGGATGACTATGATGACACAGAAAGCTCTTGAAAAAAATGGGTGGCTAG	539
Db	873	CTGTTCAATCAGTTGGATGACTATGATGACACAGAAAGCTCTTGAAAAAAATGGGTGGCTAG	932
QY	540	CACCAACGATAGAGCTGAGAGAGAACTCAAAAGTGTCTTACAAATGTTGGACCTGGCT	599
Db	933	CACCAACGATAGAGCTGAGAGAGAACTCAAAAGTGTCTTACAAATGTTGGACCTGGCT	992
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Db	993	TTAGTGGAAATTTTCTACAAAAAAGTCAGAGATGACATCCACTCTACCAATGAAGTGA	1052
QY	660	CGAACAATTTCAATGTGATAGTACTCTCAGAGAGAGCTGGAACCAAGACATATATGCA	719

Db	1053	CAAGATTTTACAAATGTGATAGGTAGTCTCAAGAGGACGTGGAAACCAAGACGATATGTCA	1112
QY	720	TTCTGGGAGGCTACCGGGACTCATGGGCTTTGGGATATGACCTCAGAGTGGAGAG	779
Db	1113	TTCTGGGAGGCTACCGGGACTCATGGGCTTTGGGATATGACCTCAGAGTGGAGAG	1172
QY	780	CTGTGTTCATGAACAACCTGTGAGGAGCTTTGGACACTGMAAAGAGGCTGAGACCTA	839
Db	1173	CTGTGTTCATGAACAATGTGAGGAGCTTTGGACACTGMAAAGAGGCTGAGACCTA	1232
QY	840	GAAGAACATTTTGTTCGCAAGCTGGGATGCAAGAATTGGTCTTCGTCTACTG	899
Db	1233	GAAGAACATTTTGTTCGCAAGCTGGGATGCAAGAATTGGTCTTCGTCTACTG	1292
QY	900	AGTGGGGCAGAGATTAATTCAGAGCTCCCTTCAAGAGCGGGCTGGCTATTTAAATGCTG	959
Db	1293	AGTGGGGCAGAGAGATTCAGAGCTCCCTTCAAGAGCGGGCTGGCTATTTAAATGCTG	1352
QY	960	ACTCATCTATAGAAAGAACTACACTCTGCAAGTTGATTTGACACCACTGATGACAGCT	1019
Db	1353	ACTCATCTATAGAAAGAACTACACTCTGCAAGTTGATTTGACACCACTGATGACAGCT	1412
QY	1020	TGCTATACACCTTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTC	1079
Db	1413	TGCTATACACACCTTAACAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTC	1472
QY	1080	TTTATGAAAGTTGGACCTMAAAAAGTCCCTTCCCAAGTTGATGATGCGATGCCAGATAA	1139
Db	1473	TTTATGAAAGTTGGACCTMAAAAAGTCCCTTCCCAAGTTGATGATGCGATGCCAGATAA	1532
QY	1140	GCAAAATTTGGAGTCTGGAATGATTTTGGAGTCTTCCCAAGCTTGGATGATGCTTCAG	1199
Db	1533	GCAAAATTTGGAGTCTGGAATGATTTTGGAGTCTTCCCAAGCTTGGATGATGCTTCAG	1592
QY	1200	GCAGAGCACGGTATTAATAAAATTGGGAACAACAAATTCAGCGGCTATCCACTGATTC	1259
Db	1593	GCAGAGCACGGTATTAATAAAATTGGGAACAACAAATTCAGCGGCTATCCACTGATTC	1652
QY	1260	ACAGTGTCTATGAACCATATGATGTTGGTGGAAAAAGTTTATGATCCAAATGTTAAATATC	1319
Db	1653	ACAGTGTCTATGAACCATATGATGTTGGTGGAAAAAGTTTATGATCCAAATGTTAAATATC	1712
QY	1320	ACCTACACTGTGGCCAGGTTTGAGAGGAGGATGGGTGGACTACAGCAATTCCAATAGGC	1379
Db	1713	ACCTACACTGTGGCCAGGTTTGAGAGGAGGATGGGTGGACTACAGCAATTCCAATAGGC	1772
QY	1380	TCCCTTTTGATTTGTCGAGATTATGCTGTACTTTTAAAGAAATGATGTCACAAAATCTACA	1439
Db	1773	TCCCTTTTGATTTGTCGAGATTATGCTGTACTTTTAAAGAAATGATGTCACAAAATCTACA	1832
QY	1440	ATATTTCTATGAACATATCACAGGAATGAAGACATACGTTTATCATTTATTTACATTT	1499
Db	1833	GTATTTCTATGAACATATCACAGGAATGAAGACATACGTTTATCATTTATTTACATTT	1892
QY	1500	TTTCTGCGATAAAAAATTTTACAGAAATTCGTTCCCAAGTTTACGAGAGAGACTCCAGAGCT	1559
Db	1893	TTTCTGCGACTAAAGATTTTACAGAAATTCGTTCCCAAGTTTACGAGAGAGACTCCAGAGCT	1952
QY	1560	TTGACAAAGACCCCAATATTGTTAAGAAATGATGAATGATCAACTATGTTTCTGAAA	1619
Db	1953	TTGACAAAGACCCCAATATTGTTAAGAAATGATGAATGATCAACTATGTTTCTGAAA	2012
QY	1620	GAGCATTTATGATTCATTAGGGTTTACCAGACAGACTTTTATAGCATGTCACTATG	1679
Db	2013	GAGCATTTATGATTCATTAGGGTTTACCAGACAGACTTTTATAGCATGTCACTATG	2072
QY	1680	CTCCAGAGGCGACAAACAAGTATCGAGGGGAGTATCCCGAGAAATTTATATGCTCGT	1739
Db	2073	CTCCAGAGGCGACAAACAAGTATCGAGGGGAGTATCCCGAGAAATTTATATGCTCGT	2132
QY	1740	TTGTATTTGAAGCAAAAGTGAACCTTCCAGAGGCTTGAGGAGATGTGAAGACAGATTT	1799

Db 2133 TTGATATTTGAAAGCAAACTGAGCCCTTCCTCAAGCCCTGGGAGGAAGTGAAGACAGATTT 2192

Qy 1800 CTGTTCAGCCTTCACAGTGCAGCAGCTGCAGACAGCTTTGAGTGAAGTACCTAAGAG 1859

Db 2193 ATGTTCAGCCTTCACAGTGCAGCAGCTGCAGACAGCTTTGAGTGAAGTACCTAAGAG 2252

Qy 1860 ATCTTTAGACAGCTCTGTATGAATTTGTGTGTATGTCACCTC--AAGAAATTAATG 1917

Db 2253 ATCTTTAGAGAAATCCGATGATTTGTGTGTATGTCACCTCAGAAAGAAATCGTAATGG 2312

Qy 1918 GTATATGATTAATTTAAATTTGGTATATTTGAATTAAGTGAATTTATATATAA 1977

Db 2313 GTATATGATTAATTTAAATTTGGTATATTTGAATTAAGTGAATTTATATATAA 2372

Qy 1978 AAAAAAAAAAAAAA 1992

Db 2373 AAAAAAAAAAAAAA 2387

RESULT 5
US-09-164-034B-1
GENERAL INFORMATION:
APPLICANT: Mincheff, Milcho S.
Zoubak, Serguei
TITLE OF INVENTION: Immunotherapy of Cancer Through Expression
of Truncated Tumor- or Tumor-Associated Antigen
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: William S. Ramsey,
Ramsey, Cook, Looper & Kurlander, LLC
STREET: 10420 Little Patuxent Parkway, Suite 250
CITY: Columbia
STATE: Maryland
COUNTRY: USA
ZIP: 21044
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/164,034B
FILING DATE: 30-Sep-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ramsey, William S.
REGISTRATION NUMBER: 32,715
REFERENCE/DOCKET NUMBER: br11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (410) 992-9660
TELEFAX: (410) 992-9540
SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-164-034B-1

Query Match 79.3%, Score 1579.4; DB 4; Length 2133;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1592; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

PH = 6,387, 898

Qy 480 CTGTTCATCCAGTTGGATTAATGATGACAGAGAGCTCTAGAAAAAATGGGTGCTCAG 539

Db 752 CTGTTCATCCAAATGGATTAATGATGACAGAGAGCTCTAGAAAAAATGGGTGCTCAG 811

Qy 540 CACCAACAGATAGAGCTGGAGAGAGAGTCTCAAAAGTGTCTCAAAATGGTGCACCTGGCT 599

Db 812 CACCAACAGATAGAGCTGGAGAGAGAGTCTCAAAAGTGTCTCAAAATGGTGCACCTGGCT 871

Qy 600 TTACTGGAACCTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAAGTGA 659

Db 872 TTACTGGAACCTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAAGTGA 931

Qy 660 CGAGAAATTTACAAATGTATAGTACTCTCAGAGAGCAGTGGAAACCAAGATATGTCA 719

Db 932 CAAGAAATTTACAAATGTATAGTACTCTCAGAGAGCAGTGGAAACCAAGATATGTCA 991

Qy 720 TTCTGGAGAGTCCACCGGAGCTCAGAGGTGTTGGTGTATTTGACCTCAGAGTGGACAG 779

Db 992 TTCTGGAGAGTCCACCGGAGCTCAGAGGTGTTGGTGTATTTGACCTCAGAGTGGACAG 1051

Qy 780 CTGTTCATGAGAACTGTGAGAGCTTTGGAACTGAAAAAGAGGAGTGGAGACCTA 839

Db 1052 CTGTTCATGAGAACTGTGAGAGCTTTGGAACTGAAAAAGAGGAGTGGAGACCTA 1111

Qy 840 GAAGAACAAATTTTGTGCAAGCTGGAGATGACAGAAATTTGTCTTGTGCTTCTACTG 899

Db 1112 GAAGAACAAATTTTGTGCAAGCTGGAGATGACAGAAATTTGTCTTGTGCTTCTACTG 1171

Qy 900 AGTGGAGAGAGATTAATTAAGACTCTCAAGAGCGGAGGAGCTTATTAATGCTG 959

Db 1172 AGTGGAGAGAGATTAATTAAGACTCTCAAGAGCGGAGGAGCTTATTAATGCTG 1231

Qy 960 ACTCATCTATGAGAGAACTACACTCTGAGAGTGTGATGACACCACTGATGACACT 1019

Db 1232 ACTCATCTATGAGAGAACTACACTCTGAGAGTGTGATGACACCACTGATGACACT 1291

Qy 1020 TGTATACAACTTAACAAAGAGCTGAAAAGCCTGATGAAGGCTTTGAAGCAATCTC 1079

Db 1292 TGTATACAACTTAACAAAGAGCTGAAAAGCCTGATGAAGGCTTTGAAGCAATCTC 1351

Qy 1080 TTTATGAAGTTGAGCTAAAAAAAGTCTCCAGAGTTCAGTGGGATGCCAGGATTA 1139

Db 1352 TTTATGAAGTTGAGCTAAAAAAAGTCTCCAGAGTTCAGTGGGATGCCAGGATTA 1411

Qy 1140 GCAAAATGGAGATCTGAAATGATTTGAGAGTGTCTTCCAAAGCACTTGAATTCCTCAG 1199

Db 1412 GCAAAATGGAGATCTGAAATGATTTGAGAGTGTCTTCCAAAGCACTTGAATTCCTCAG 1471

Qy 1200 GCAGAGCAGGTAATTAATAAATTTGGAAACAAATTCAGCGGCTATCCACTGTATC 1259

Db 1472 GCAGAGCAGGTAATTAATAAATTTGGAAACAAATTCAGCGGCTATCCACTGTATC 1531

Qy 1260 ACAATGCTATGAAGCAATATAGTGTGGGAAAGTTTATGATCCAAATGTTAAATATC 1319

Db 1532 ACAATGCTATGAAGCAATATAGTGTGGGAAAGTTTATGATCCAAATGTTAAATATC 1591

Qy 1320 ACCTCAGCTGTGGCCAGGTTTCAGAGAGAGATGTGTTGAGCTGAGCAATTCATAGTGC 1379

Db 1592 ACCTCAGCTGTGGCCAGGTTTCAGAGAGAGATGTGTTGAGCTGAGCAATTCATAGTGC 1651

Qy 1380 TCCTTTTGAATGTCAGAGATTATGCTGTAGTTTAAAGAAATATGTCGACAAATCTACA 1439

Db 1652 TCCTTTTGAATGTCAGAGATTATGCTGTAGTTTAAAGAAATATGTCGACAAATCTACA 1711

Qy 1440 ATATTTCTATGAACATCCAGAGAAATGAAGACATACAGTTTTCATTTGATTCACATT 1499

Db 1712 GTATTTCTATGAACATCCAGAGAAATGAAGACATACAGTTTTCATTTGATTCACATT 1771

Qy 1500 TTTCTGACGTAATAAATTTTACAGAAATTTGCTTCAAGTTCAGGAGAGACTCCAGAGCT 1559

Db 1772 TTTCTGACGTAATAAATTTTACAGAAATTTGCTTCAAGTTCAGGAGAGACTCCAGAGCT 1831

SEQUENCE CHARACTERISTICS:
LENGTH: 893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEITICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-45

Query Match 11.2%; Score 223.2; DB 2; Length 893;
Best Local Similarity 92.8%; Pred. No. 8.6e-50;
Matches 256; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 1 AGCAATACCTACCTACCAATTAAGAATTCCTCAATCTGATGTTCTGAGATTCTTA 60
DB 275 AGCAATACCTACCTACCAATTAAGAATTCCTCAATCTGATGTTCTGAGATTCTTA 216
QY 61 GAGCTTATAGTACGAAAAAGGAAATTCCTCTGAGATCTCTTTTGTAGGCC 120
DB 215 CAGCTTATAGTACGAAAAAGGAAATTCCTCTGAGATCTCTTTTGTAGGCC 157
QY 121 TAAAGA-CAAAAGTTGAGATAAGTTCTAGTACTCATTTAAGTGAATTAATTT 179
DB 156 TAAAGAGAAAAGTTGAGATAAGTTCTAGTACTCATTTAAGTGAATTTAAAAATTT 97
QY 180 GATATTACCAATCTGCAACCAATTTAAATTAAGAAAGAAAGACACTGTCTTCT 239
DB 96 GATATTACCAATCTGCAACCAATTTAAATTAAGAAAGAAAGACACTGTCTTAACT 37
QY 240 AGGTTAAATGCCCCAGCTGCGAGGCGCAAGAG 275
DB 36 AGGTTAAATGCCCCAGCTGCGAGGCGCAAGAG 1

RESULT 9
US-09-439-313-454/c
; Sequence 454, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 454
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-454

Query Match 11.1%; Score 220.2; DB 4; Length 231;
Best Local Similarity 98.7%; Pred. No. 2.9e-49;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 778 AGCTGTTGTCATGAACCTGTGAGAGCTTTGGACACTGAAAAAGAGGTGAGACC 837
DB 231 AGCTGTTGTCATGAACCTGTGAGAGCTTTGGACACTGAAAAAGAGGTGAGACC 172
QY 838 TAGAAGACAAATTTGTTTGCAGCTGAGATGCAAGAAATTTGCTTCTTGCTCTAC 897
DB 171 TAGAAGACAAATTTGTTTGCAGCTGAGATGCAAGAAATTTGCTTCTTGCTCTAC 112
QY 898 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATATTAATGC 957
DB 111 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATATTAATGC 52
QY 958 TGACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTGTAC 1002
DB 51 TGACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTGTAC 7

RESULT 10
US-09-352-616A-454/c
; Sequence 454, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 454
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-352-616A-454

Query Match 11.1%; Score 220.2; DB 4; Length 231;
Best Local Similarity 98.7%; Pred. No. 2.9e-49;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 778 AGCTGTTGTCATGAACCTGTGAGAGCTTTGGACACTGAAAAAGAGGTGAGACC 837
DB 231 AGCTGTTGTCATGAACCTGTGAGAGCTTTGGACACTGAAAAAGAGGTGAGACC 172
QY 838 TAGAAGACAAATTTGTTTGCAGCTGAGATGCAAGAAATTTGCTTCTTGCTCTAC 897
DB 171 TAGAAGACAAATTTGTTTGCAGCTGAGATGCAAGAAATTTGCTTCTTGCTCTAC 112
QY 898 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATATTAATGC 957
DB 111 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATATTAATGC 52
QY 958 TGACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTGTAC 1002
DB 51 TGACTCATCTATAGAAAGAACTACACTCTGAGAGTTGATTGTAC 7

RESULT 11
US-08-325-553-27
; Sequence 27, Application US/08325553
; Patent No. 5538866
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Cooper & Dunham

	Matches	267;	Conservative	0;	Mismatches	218;	Indels	10;	Gaps	5;
QY	620	CAAAAAGTCAAGATGACATCCACTCTACCATGAGTACAGAGATTTTACATGTGATA	679							
Db	89	CAAAATGTGAAGCTCAGTGTGAACAATGTAAGAAACAAATACCTTACATCTT	148							
QY	680	GGTACTCTCAGAGGAGGAGCAACACAGATATGTCACTTGTGGAGGTACCGGAC	739							
Db	149	GGCGTATTAAGGCTATGAGGAGACAGACCGCTACATTTGATGAGAGCCACAGAGAC	208							
QY	740	TCATGGGTGTTGGTATTTGACCCCTCAGAGT-GGAGCAGCTGTGTTCATGAACTGT	798							
Db	209	GCTTGGGGCCCTGGTGTGGAGTCCAGTGTGGAAACAGGCTTCTTGTGAACTTG	268							
QY	799	GAGGAGCTTTGGAACACTGAA---AAGGAAGGGTGGAGACTGAGAAGAAATTTGT	854							
Db	269	CCCAAGTATTTCTCAGATATGATTTCAAAAGATGATTTAGACCAGAGAGTATATCT	328							
QY	855	TTGCAAGCTGGAGATGCAAGAGATTTGGCTTTTGGTTCTACTGAGTGGCAGAGC---	911							
Db	329	TTGCCAGCTGGACTGAGAGACTATGTAGCTGTTGGTCCGACTGAGTGGCTGGAGGGGT	388							
QY	912	ATAATTCAGAGCTCCTTCAAGAGGGGCGTGTATTAATGCTGACTCATCTATAG	971							
Db	389	ACCTTCACTCTTTCATCTTAAGNNNGCTTCACTTACATTAATCTGGATAAAGTCGTC	448							
QY	972	AAGGAACCTA-CACCTGAGAGTTGATTTGACACCACTGATGTACAGCTTGATACAAAC	1030							
Db	449	CTGGGTACTACCACTTCAAGCTTTCTGCCAGCCCCCTATATATACACTTATGGGGAG	508							
QY	1031	CTAACAAGAGCTGAAAAGC-CCTGATGAAGGCTTTGAGGCAATCTCTTATGAAG	1089							
Db	509	ATAATGCAGGANNNGTAAAGCATCCGANNNNNNNTTGATGAAAATATCTATATCGAAA	568							
QY	1090	TTGACTTAAAAAAG	1104							
Db	569	CAGTATTTGGATTAG	583							

Search completed: October 4, 2003, 20:58:28
Job time : 182 secs

Db 1019 TCCAGCGTGGAAATATCCTAATCTGATGTGTGAGAGAACCCCTCTCACACAGGTTACC 1078
Qy 420 CAGCAAAATGAATACGCTTATAGCGATGAAATGCGAGAGCGTGTGGTCTCCAAAGTATTC 479
Db 1079 CAGAAATGAATATGCTTATAGCGATGAAATGCGAGAGCGTGTGGTCTCCAAAGTATTC 1138
Qy 480 CTGTTCATCCAGTTGGATCTACTATGATGACAGAAAGCTCCCTAGAAAAATGGGTGGCTCAG 539
Db 1139 CTGTTCATCCAAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1198
Qy 540 CACCACAGATAGACGCTGAGAGAGAGATCTCAAAAGTGTCTTACAAATGTTGAGACCTGGCT 599
Db 1199 CACCACAGATAGACGCTGAGAGAGAGATCTCAAAAGTGTCTTACAAATGTTGAGACCTGGCT 1258
Qy 600 TTACTGGAACCTTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAAGTGA 659
Db 1259 TTACTGGAACCTTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAAGTGA 1318
Qy 660 CGAGAATTTACATGTATAGTACTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Db 1319 CAAAGAAATTTACAAATGATAGTACTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1378
Qy 720 TTCTGGGAGGTCACCGGACCTCATGGGTGTGGTGTATGATGACCTCAGAGTGGAGCAG 779
Db 1379 TTCTGGGAGGTCACCGGACCTCATGGGTGTGGTGTATGATGACCTCAGAGTGGAGCAG 1438
Qy 780 CTGTTGTTTCATGAACCTGTGAGAGAGCTTTGGACACTGAAAAAGAGAGGTGAGACCTA 839
Db 1439 CTGTTGTTTCATGAACCTGTGAGAGAGCTTTGGACACTGAAAAAGAGAGGTGAGACCTA 1498
Qy 840 GAAACAAATTTTGTGGCAAGCTGGGATGCGAAGAAATTTGGTCTTCTGTTCTACTG 899
Db 1499 GAAACAAATTTTGTGGCAAGCTGGGATGCGAAGAAATTTGGTCTTCTGTTCTACTG 1558
Qy 900 AGTGGGCGAGGATATATCAAGACTCCTCAAGAGCGGCGGCTATATATATGCTG 959
Db 1559 AGTGGGCGAGGATATATCAAGACTCCTCAAGAGCGGCGGCTATATATATGCTG 1618
Qy 960 ACTCATCTATAGAAAGAACTACACTGTGAGAGTTGATTTGACACCACTGATGTACAGCT 1019
Db 1619 ACTCATCTATAGAAAGAACTACACTGTGAGAGTTGATTTGACACCACTGATGTACAGCT 1678
Qy 1020 TGGTATACAACTTAACAAAAGCTGAAAAGCCCTGATGAGAGGCTTTGAAGGCAAAATCTC 1079
Db 1679 TGGTATACAACTTAACAAAAGCTGAAAAGCCCTGATGAGAGGCTTTGAAGGCAAAATCTC 1738
Qy 1080 TTTATGAAAGTTGGCAATAAAAAGTCTCCCAAGATGTGATGCGATGCGCCAGATTA 1139
Db 1739 TTTATGAAAGTTGGCAATAAAAAGTCTCCCAAGATGTGATGCGATGCGCCAGATTA 1798
Qy 1140 GCAAAATGGGATCTGGAATGATTTTGGAGTGTCTTCCAAAGATGGAATGCTTCCAG 1199
Db 1799 GCAAAATGGGATCTGGAATGATTTTGGAGTGTCTTCCAAAGATGGAATGCTTCCAG 1858
Qy 1200 GCAGAGCAGGATTAACAAAATGGAACAAAACAAAATGAGCGGCTATCCACAGTATC 1259
Db 1859 GCAGAGCAGGATTAACAAAATGGAACAAAACAAAATGAGCGGCTATCCACAGTATC 1918
Qy 1260 ACAGTGTCTATGAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1319
Db 1919 ACAGTGTCTATGAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1378
Qy 1320 ACCTCACTGTGGCCAGGTTGAGAGAGGATGTTGTTGAGCTAGCCAAATTCATAGTGC 1379
Db 1979 ACCTCACTGTGGCCAGGTTGAGAGAGGATGTTGTTGAGCTAGCCAAATTCATAGTGC 2038
Qy 1380 TCCCTTTGATGTTGCGAGATTAATGCTGATGTTTAAAGAAAGTATGCTGACAAAATCTACA 2098
Db 2039 TCCCTTTGATGTTGCGAGATTAATGCTGATGTTTAAAGAAAGTATGCTGACAAAATCTACA 2098
Qy 1440 ATATTTCTATGAACATCCACAGAGAAATGAGACATACATGTTATCATTTGATTCACATT 1499
Db 2099 GTATTTCTATGAACATCCACAGAGAAATGAAAGACATACAGTGTATCATTTGATTCACATT 2158

Qy 1500 TTTCTGAGTAAAAATTTTACGAATATGCTTCCAGATTTGAGAGAGAGAGAGAGAGAGACT 1559
Db 2159 TTTCTGAGTAAAAATTTTACGAATATGCTTCCAGATTTGAGAGAGAGAGAGAGAGACT 2218
Qy 1560 TTGCAAAAGCAACCCCAATATTTGTTAAGATGATGATGATGATGATGATGATGATGATGATG 1619
Db 2219 TTGCAAAAGCAACCCCAATATTTGTTAAGATGATGATGATGATGATGATGATGATGATGATG 2278
Qy 1620 GAGCATTTATGATTCATTAAGGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1679
Db 2279 GAGCATTTATGATTCATTAAGGTTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2338
Qy 1680 CTCACAG 1739
Db 2339 CTCACAG 2398
Qy 1740 TTGATTTTGAAGCAAGAGTGGACCTTCCAAAGGCTGGGAGATGTAAGAGAGAGAGATTT 1799
Db 2399 TTGATTTTGAAGCAAGAGTGGACCTTCCAAAGGCTGGGAGATGTAAGAGAGAGAGATTT 2458
Qy 1800 CTGTTGACGCTTACAGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1859
Db 2459 ATGTTGACGCTTACAGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2518
Qy 1860 ATTCTTAAAGAGCTCTGATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1917
Db 2519 ATTCTTAAAGAGCTCTGATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2578
Qy 1918 GTATATGATTAATTTTAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1977
Db 2579 GTATATGATTAATTTTAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2638
Qy 1978 AAAAAAAAAAAAAA 1992
Db 2639 AAAAAAAAAAAAAA 2653

RESULT 2
US-09-873-319-451
; Sequence 451, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Mungler, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Gelzenderg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; CURRENT FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 M99487
US-09-873-319-451

Query Match 85.5%; Score 1702.6; DB 12; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
Qy 240 AGTTTAAAAATGCCAGCTGCGAGGGGCAAGAGAGTATTTCTACTACAGACCTGCTG 299
Db 899 AGTTTAAAAATGCCAGCTGCGAGGGGCAAGAGAGTATTTCTACTACAGACCTGCTG 958

QY 300 ACTACTTTGCTCCCTGGGGTGAAGTCCCTATCCAGACGGTTGGAATCTTCTCGAGAGTGTG 359
 |||||
 Db 959 ACTACTTTGCTCCCTGGGGTGAAGTCCCTATCCAGATGTTGGAATCTTCTCGAGAGTGTG 1018
 |||||
 QY 360 TCCAGCGTGGAAATATCTTAATCTGAATGTCGAGAGAACCTCTCACACCGATTACC 419
 |||||
 Db 1019 TCCAGCGTGGAAATATCTTAATCTGAATGTCGAGAGAACCTCTCACACCGATTACC 1078
 |||||
 QY 420 CAGCAATGAAATACGTTATAGGATGAAATGCAAGGCTGTGTCTTCCAGATTTC 479
 |||||
 Db 1079 CAGCAATGAAATATGTTATAGGCTGGAATGCAAGGCTGTGTCTTCCAGATTTC 1138
 |||||
 QY 480 CTGTTTCATCCAGTTGGATACATATGATGACAGAGCTCTAGAAAAAATGGTGGCTCAG 539
 |||||
 Db 1139 CTGTTTCATCCAGTTGGATACATATGATGACAGAGCTCTAGAAAAAATGGTGGCTCAG 1198
 |||||
 QY 540 CACACACAGATAGCAGCTGGAGAGAGATCTCAAAATGTCCTACATGTTGGACCTGGCT 599
 |||||
 Db 1199 CACACACAGATAGCAGCTGGAGAGAGATCTCAAAATGTCCTACATGTTGGACCTGGCT 1258
 |||||
 QY 600 TTAGTGAAGAACTTTCTACAAAAAGTCAAGATGCATCCACTACCAATGAAGTGA 659
 |||||
 Db 1259 TTAGTGAAGAACTTTCTACAAAAAGTCAAGATGCATCCACTACCAATGAAGTGA 1318
 |||||
 QY 660 CGAGAAATTTACATGTATAGTACTCTCAGAGAGCAGTGAACCGACAGATATGTCA 719
 |||||
 Db 1319 CGAGAAATTTACATGTATAGTACTCTCAGAGAGCAGTGAACCGACAGATATGTCA 1378
 |||||
 QY 720 TTCTGGAGAGTACCGGGACTCATGGGTGTTGGTGTATGACCTCAGATGGAGCAG 779
 |||||
 Db 1379 TTCTGGAGAGTACCGGGACTCATGGGTGTTGGTGTATGACCTCAGATGGAGCAG 1438
 |||||
 QY 780 CTGTTGTTATGAAACTGTGAGAGGCTTGAACAACCTGAAAAAGGATGGAGACTA 839
 |||||
 Db 1439 CTGTTGTTATGAAATTTGAGAGAGCTTTGGAACCTGAAAAAGGATGGAGACTA 1498
 |||||
 QY 840 GAGAAACAATTTGTTGTCAGAGCTGGAGTCAAGAAATTTGGTCTCTCTGTTCTACTG 899
 |||||
 Db 1499 GAGAAACAATTTGTTGTCAGAGCTGGAGTCAAGAAATTTGGTCTCTCTGTTCTACTG 1558
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 QY 900 AATGGGCGAGAGATATTTCAAGACTCTCTCAAGAGCGTGGCTTATTTAATGCTG 959
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 Db 1559 AATGGGCGAGAGATTTCAAGACTCTCTCAAGAGCGTGGCTTATTTAATGCTG 1618
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 QY 960 ACTCATCTATAGAGAACTACACCTGAGAGTTGATGTATACACCATGATGTACAGCT 1019
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 Db 1619 ACTCATCTATAGAGAACTACACCTGAGAGTTGATGTATACACCATGATGTACAGCT 1678
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 QY 1020 TGGTATACAACTTAACAAAAAGCTGAAAAAGCCCTGATGAAGCTTTGAAGCAATCTC 1079
 |||||
 Db 1679 TGGTATACAACTTAACAAAAAGCTGAAAAAGCCCTGATGAAGCTTTGAAGCAATCTC 1738
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 QY 1080 TTTATGAAGTGGAGCTAAAAAAGTCCCTCCAGAGTTCAGTGGCATGCCAGATTA 1139
 |||||
 Db 1739 TTTATGAAGTGGAGCTAAAAAAGTCCCTCCAGAGTTCAGTGGCATGCCAGATTA 1798
 |||||
 QY 1140 GCAAAATGGAGATCGAAATGATTTTGAAGTGTCTTCCACAGACTTGAATTTGCTCAG 1199
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 Db 1799 GCAAAATGGAGATCGAAATGATTTTGAAGTGTCTTCCACAGACTTGAATTTGCTCAG 1858
 |||||
 QY 1200 GCAGAGCAGGTATACATAAAATTTGGAAAAACAACAAATTCAGCGCTATCCACTGATC 1259
 |||||
 Db 1859 GCAGAGCAGGTATACATAAAATTTGGAAAAACAACAAATTCAGCGCTATCCACTGATC 1918
 |||||
 QY 1260 ACAGTGTCTATGAACATATGAGTGTGGAAAAAGTTTATGATCCAAATGTTAATATC 1319
 |||||
 Db 1919 ACAGTGTCTATGAACATATGAGTGTGGAAAAAGTTTATGATCCAAATGTTAATATC 1978
 |||||
 QY 1320 ACCCTACGTGGCCAGGTTTCAGAGAGGAGTGTGTTTGAAGTCCATTTCCATGTCG 1379
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 Db 1979 ACCCTACGTGGCCAGGTTTCAGAGAGGAGTGTGTTTGAAGTCCATTTCCATGTCG 2038
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 QY 1380 TCCCTTTGATGTTGAGATATATGCTAGTTTAAAGAAATATGCTGACAAATCTACA 1439
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Db 2039 TCCCTTTGATGTTGAGATTTATGCTGTGATTTTGAAGAAATGCTGACAAATCTACA 2098
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 QY 1440 ATATTTCTATGAACATCCACAGAGAAATGAAGCATACAGTTATATTTGATTCCTT 1499
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 Db 2099 ATATTTCTATGAACATCCACAGAGAAATGAAGCAATGATATATTTGATTCCTT 2158
 |||||
 QY 1500 TTTCTGACGTAAAAAATTTTACAGAAATGCTTCCAGTTCAGCGAGAGCTCAGAGCT 1559
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 Db 2159 TTTCTGACGTAAAAAATTTTACAGAAATGCTTCCAGTTCAGTTCAGTTCAGAGCT 2218
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 QY 1560 TTGACAAAAACAACCAATATTTTAAAGATGATGAATGATCACTCATGTTCTGAAA 1619
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 Db 2219 TTGACAAAAACAACCAATATTTTAAAGATGATGAATGATCACTCATGTTCTGAAA 2278
 |||||
 QY 1620 GAGCATTTATGATTCATAGGTTACGACAGACACTTTTATAGGATGTCATATG 1679
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 Db 2279 GAGCATTTATGATTCATAGGTTACGACAGACACTTTTATAGGATGTCATATG 2338
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 QY 1680 CTCACAGACCAACAAGATATGACAGGAGATTCACAGAAATTTATGATGCTCTGT 1739
 |||||
 Db 2339 CTCACAGACCAACAAGATATGACAGGAGATTCACAGAAATTTATGATGCTCTGT 2398
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 QY 1740 TTGATTTGAAGCAAAAGTGAACCTTCCAGGCTGGGAGATGTGAAGACAGATTT 1799
 |||||
 Db 2399 TTGATTTGAAGCAAAAGTGAACCTTCCAGGCTGGGAGATGTGAAGACAGATTT 2458
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 QY 1800 CTGTTGACCTTTCACAGTGCAGAGGCTGTCAGAGACTTTGATGAAGTACGTAAGAG 1859
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 Db 2459 ATGTTGACCTTTCACAGTGCAGAGGCTGTCAGAGACTTTGATGAAGTACGTAAGAG 2518
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 QY 1860 ATTCTTTAGAGACTGTATGATTTGTTGTTGATATGCTACATC -AAGAAATATATG 1917
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 Db 2519 ATTCTTTAGAGACTGTATGATTTGTTGTTGATATGCTACATCAGAAAGTATATG 2578
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 QY 1918 GATATTTGATTAATTTTAAATTTGATTTGATTTGATTTGATTTGATTTGATTTA 1977
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 Db 2579 GATATTTGATTAATTTTAAATTTGATTTGATTTGATTTGATTTGATTTGATTTA 2638
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 QY 1978 AAAAAAAAAAAAAA 1992
 |||||
 Db 2639 AAAAAAAAAAAAAA 2653
 |||||

RESULT 3
 ; US-09-960-706-716
 ; Sequence 716, Application US/09960706
 ; Publication No. US20030134280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mungier, William E.
 ; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperp
 ; FILE REFERENCE: 44921-5029-01US
 ; CURRENT APPLICATION NUMBER: US/09/960, 706
 ; CURRENT FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 60/223, 323
 ; PRIOR FILING DATE: 2000-08-07
 ; PRIOR APPLICATION NUMBER: 09/873, 319
 ; PRIOR FILING DATE: 2001-06-05
 ; NUMBER OF SEQ ID NOS: 1124
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 716
 ; LENGTH: 2653
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20030134280A1 M59487
 ; US-09-960-706-716

Query Match 85.5%; Score 1702.6; DB 12; Length 2653;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY	240	AGGTTAAATTAATGGCCACCTGGACGGGGCCAAAGAGATCATTTCTACTCGACCCCTCTG	299
Db	899	AGGTTAAATTAATGGCCACCTGGACGGGGCCAAAGAGATCATTTCTACTCGACCCCTCTG	958
QY	300	ACTACTTTCCTCTGGGGTGAAGTCCATTCACAGCGGTTTGGAAATCTTCTCGAGAGTGCTG	359
Db	959	ACTACTTTCCTCTGGGGTGAAGTCCATTCACAGCGGTTTGGAAATCTTCTCGAGAGTGCTG	1018
QY	360	TCCAGCGTGGAAATATCTTAAATCTGAATGTGACAGAGACCTCTACACACAGTTTACC	419
Db	1019	TCCAGCGTGGAAATATCTTAAATCTGAATGTGACAGAGACCTCTACACACAGTTTACC	1078
QY	420	CAGCAAAATGAAATACGCTTATAGGCAATGGAATTTGAGAGGCGTTTGTCCTCAAGTATTC	479
Db	1079	CAGCAAAATGAAATATGCTTATAGGCGTGGAAATTTGAGAGGCGTTTGTCCTCAAGTATTC	1138
QY	480	CTGTTCATCCAGTTGGATGATCTATGATCACAAGAGCTCCTAGAAAAAATGGGTGGCCACG	539
Db	1139	CTGTTCATCCAGTTGGATGATCTATGATCACAAGAGCTCCTAGAAAAAATGGGTGGCCACG	1198
QY	540	CACCACACAGATAGCAGCTGGAGAGGAAGTCTCAAAAGTCCCTACATATGTTGGACTGGCT	599
Db	1199	CACCACACAGATAGCAGCTGGAGAGGAAGTCTCAAAAGTCCCTACATATGTTGGACTGGCT	1258
QY	600	TTTACTGGAAACTTTTCTACACAAAAAATCCAAAGATGCACATCCACTACCAATCAATGATGA	659
Db	1259	TTTACTGGAAACTTTTCTACACAAAAAATCCAAAGATGCACATCCACTACCAATCAATGATGA	1318
QY	660	CGAAGAAATTCACATGTATGATAGTACTCTCAGAGAGCAGAGTGAACACAGACAGATATGTCA	719
Db	1319	CGAAGAAATTCACATGTATGATAGTACTCTCAGAGAGCAGAGTGAACACAGACAGATATGTCA	1378
QY	720	TTCTGGGAGGTACACGGGACTCATGGGTGTTTGGGTATTTGACCTTCAGAGTGGACAG	779
Db	1379	TTCTGGGAGGTACACGGGACTCATGGGTGTTTGGGTATTTGACCTTCAGAGTGGACAG	1438
QY	780	CTGTGTTTTCATGAACACTGTGAGAGCTTTGGAACTGAAAAAAGGAAGGGTGGAGACTTA	839
Db	1439	CTGTGTTTTCATGAACAAATGTGTGAGAGCTTTGGAACTGAAAAAAGGAAGGGTGGAGACTTA	1498
QY	840	GAAGAACAAATTTTGTTCGCAAGCTGGGAGTGCAGAGAAATTTGTGCTTCTTGTTCTACTG	899
Db	1499	GAAGAACAAATTTTGTTCGCAAGCTGGGAGTGCAGAGAAATTTGTGCTTCTTGTTCTACTG	1558
QY	900	AGTGGGACAGAGATTAATTCAGACTCCTTCAAGAGCGTGGCGGCTTATATTAATGCTG	959
Db	1559	AGTGGGACAGAGATTAATTCAGACTCCTTCAAGAGCGTGGCGGCTTATATTAATGCTG	1618
QY	960	ACTCATCTATAGAAGGAACCTACACTCTGAGAGTGTGATTTGACACCACTGATGTACAGCT	1019
Db	1619	ACTCATCTATAGAAGGAACCTACACTCTGAGAGTGTGATTTGACACCACTGATGTACAGCT	1678
QY	1020	TGATATTCACACCTTAACAAAAGAGCTGAAAAACCCCTGATGAAGGGCTTGAAGCAAGAAATCTC	1079
Db	1679	TGATATTCACACCTTAACAAAAGAGCTGAAAAACCCCTGATGAAGGGCTTGAAGCAAGAAATCTC	1738
QY	1080	TTTATGAAAGTTGAGCTAAAAAAAAGTCCCTTCCCGAAGTTCAAGTGGCATGCGCCACGATTA	1139
Db	1739	TTTATGAAAGTTGAGCTAAAAAAAAGTCCCTTCCCGAAGTTCAAGTGGCATGCGCCACGATTA	1798
QY	1140	GCAAAATTTGGGATCTGGAAATGATTTTGAAGTGTCTTCCAAACGACTTGGAAATGCTCTCAG	1199
Db	1799	GCAAAATTTGGGATCTGGAAATGATTTTGAAGTGTCTTCCAAACGACTTGGAAATGCTCTCAG	1858
QY	1200	GCAGAGCAGCGGTATACCTAAAAAATTTGGGAAACAAACAAATTAAGGGGCTATCCACTGATTC	1259
Db	1859	GCAGAGCAGCGGTATACCTAAAAAATTTGGGAAACAAACAAATTAAGGGGCTATCCACTGATTC	1918
QY	1260	ACAGTGTCTATGAACACATATGATGTTGGGAAAAAGTTTATGATCCAAATGTTTAAATATTC	1319
Db	1919	ACAGTGTCTATGAACACATATGATGTTGGGAAAAAGTTTATGATCCAAATGTTTAAATATTC	1978
QY	1320	ACCTCACTGTGGCCCGAGGCTTCAGAGAGGGATGTGTTGAGCTACCCAAATTCATATGCTGC	1379

Db	1979	ACCTCACTGtGGCCAGGTTcGAGGAGGATGtGGTTGAGcTfAGCCAAATTCATAGTGC	2038
Qy	1380	TCCCTTTTGATtGTCCGAGATTATGCTAGTTTTAAAGATATGCTGCACAAATCTACA	1439
Db	2039	TCCCTTTTGATtGTGCGGATTAATGCTGATTTTTAAAGATATGCTGCACAAATCTACA	2098
Qy	1440	ATATTTCTATGAAGAAATCCACAGAAATGAAGACATfCAGTTTATCAATTTGATTCACGTTT	1499
Db	2099	GTAATTTCTATGAAGAAATCCACAGAAATGAAGACATfCAGTGTATCAATTTGATTCACGTTT	2158
Qy	1500	TTTTCTGCAGTAAAAAATTTTACAGAAATTCCTTCCAGTTTCAGCGAGAGACTCCAGACT	1559
Db	2159	TTTTCTGCAGTAAAAAATTTTACAGAAATTCCTTCCAGTTTCAGCGAGAGACTCCAGACT	2218
Qy	1560	TTGACAAAGCAACCCCAATfTTGTTAAGATGATGAATGATCAACTATGTTTGTGAAA	1619
Db	2219	TTGACAAAGCAACCCCAATfAGTATTAGAAATGATGAATGATCAACTATGTTTGTGAAA	2278
Qy	1620	GAGATTTATTTGAATTCCTTAGGGGTTTACCAGACAGACTTTTATATAGGCATGCTATATG	1679
Db	2279	GAGATTTATTTGAATTCCTTAGGGGTTTACCAGACAGACTTTTATATAGGCATGCTATATG	2338
Qy	1680	CTCCAACGACGACCAACAAGATATGACAGGGAGTCAATTCACAGAAATTTATGATGCTCTGT	1739
Db	2339	CTCCAACGACGACCAACAAGATATGACAGGGAGTCAATTCACAGAAATTTATGATGCTCTGT	2398
Qy	1740	TTGATATTGGAAGCAAGAGTGAGCCCTTCCAAAGCCTTGCGGAGATGTGAAGACAGATTT	1799
Db	2399	TTGATATTGGAAGCAAGAGTGAGCCCTTCCAAAGCCTTGCGGAGATGTGAAGAGACAGATTT	2458
Qy	1800	CTGTGAGGCTTCACAGTGCAGGCACTGTCAGAGACTTTGAGAGAAATGACTCTCAAGAG	1859
Db	2459	ATGTTTGAGGCTTCACAGTGCAGGCACTGTCAGAGACTTTGAGAGAAATGACTCTCAAGAG	2518
Qy	1860	ATTCTTTAGAGACTCTGATTTGAATTTGTGTATGTCACTC--AAAGAAATAATG	1917
Db	2519	ATTCTTTAGAGAAATCCGATATTGATTTGTGTATGTCACTCAGAAAGAAATCGAATAG	2578
Qy	1918	GTAATATTGATTAATTTTAAAAATTTGCTATTTTGAATTAAGTTGAATTTTATATATAAA	1977
Db	2579	GTAATATTGATTAATTTTAAAAATTTGCTATATTGGAATTAAGTTGAATTTTATATATAAA	2638
Qy	1978	AAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAA 2653	
RESULT 4			
US-10-210-120-5			
: Sequence 5, Application US/10210120			
: Publication No. US20030175736A1			
: GENERAL INFORMATION:			
: APPLICANT: Chinnaiyan, Arul M.			
: APPLICANT: Rudin, Mark A.			
: APPLICANT: Sreekumar, Arun			
: TITLE OF INVENTION: Expression Profile of Prostate Cancer			
: FILE REFERENCE: UM-07221			
: CURRENT APPLICATION NUMBER: US/10/210.120			
: CURRENT FILING DATE: 2002-08-01			
: PRIOR APPLICATION NUMBER: US 60/309,581			
: PRIOR FILING DATE: 2001-08-02			
: PRIOR APPLICATION NUMBER: US 60/334,468			
: PRIOR FILING DATE: 2001-11-15			
: NUMBER OF SEQ ID NOS: 123			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 5			
: LENGTH: 2653			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
US-10-210-120-5			
Query Match	85.5%	Score 1702.6;	DB 12; Length 2653;

Db	1919	ACAGTGTCTATTAACAAACATATGATGATGGTGGGAAAGATTTTATGATCCAAAGTTTTAAATATAC	1978
QY	1320	ACCTGCATGTGGCCCGAGTTTCAGAGGAGGATGGTCTTTAGGTCAGCAATTCATATGATGC	1379
Db	1979	ACCTCACTGTGGCCCGAGTTTCAGAGGAGGATGGTCTTTAGGTCAGCAATTCATATGATGC	2038
QY	1380	TCCCTTTTGATTTGTGCAGATTTATAGCTAGTATTTTAAAGAAAGTATGCTGCAAAATCTACA	1439
Db	2039	TCCCTTTTGATTTGTGCAGATTTATAGCTAGTATTTTAAAGAAAGTATGCTGCAAAATCTACA	2098
QY	1440	ATATTTTCTATGAACATCCACAGGAATGAAGACATACAGTTTATCATTTGATTCCTTT	1499
Db	2099	GATTTTCTATGAACATCCACAGGAATGAAGACATACAGTTTATCATTTGATTCCTTT	2158
QY	1500	TTTTCTGCAGTAAATAATTTTACGAATAATGCTTCCAAAGTTCACGGAGAGCTCCAGAGCT	1559
Db	2159	TTTTCTGCAGTAAATAATTTTACGAATAATGCTTCCAAAGTTCACGGAGAGCTCCAGAGCT	2218
QY	1560	TTGACAAAAGCACCACCAATATGTTGAAGATGATGATGATCAACATCATGTTTCTGAAA	1619
Db	2219	TTGACAAAAGCACCACCAATATGTTGAAGATGATGATGATCAACATCATGTTTCTGAAA	2278
QY	1620	GACCATTTATTTGATTCATTAGGGTTACACAGACAGACCTTTTATAGCATGTCATCTATG	1679
Db	2279	GACCATTTATTTGATTCATTAGGGTTACACAGACAGACCTTTTATAGCATGTCATCTATG	2338
QY	1680	CTCCAAAGCAGCCACCAACAGTATGCAAGGGAGATTCATCCAGGAATTTATGATGCTCTGT	1739
Db	2339	CTCCAAAGCAGCCACCAACAGTATGCAAGGGAGATTCATCCAGGAATTTATGATGCTCTGT	2398
QY	1740	TTGATATTTGAACCAAAAGTGGACCCCTCCAAAGCCTGGGAGATGTGAAGACAGACATTT	1799
Db	2399	TTGATATTTGAACCAAAAGTGGACCCCTCCAAAGCCTGGGAGAGTGAAGACAGACATTT	2458
QY	1800	CTGTTCGACGCTTCACAGTGCAGGACGCTGCAGAGACTTTGAATGAATAGCTTAAGAGG	1859
Db	2459	ATGTGGACGCTTCACAGTGCAGGACGCTGCAGAGACTTTGAATGAATAGCTTAAGAGG	2518
QY	1860	ATTCTTTAGAGACTCTGTATTTGAATTTGTGTGTGTGTCTACTC--AAAGATATATAATGG	1917
Db	2519	ATTCTTTAGAGAAATCCGTATTTGAATTTGTGTGTGTGTCTACTCAGAAAGATGTATATGG	2578
QY	1918	GTAATATTTGAATAATTTTAAATAATGGTATATTTTGAATAAAGTTGAATATTTATATATAA	1977
Db	2579	GTAATATTTGAATAATTTTAAATAATGGTATATTTTGAATAAAGTTGAATATTTATATATAA	2638
QY	1978	AAAAAAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAAAAAA 2653	
RESULT 6			
US-10-205-823-131			
Sequence 131, Application US/10205823			
Publication No. US20030108963A1			
GENERAL INFORMATION:			
APPLICANT: Schlegel, Robert			
APPLICANT: Monahan, John E.			
APPLICANT: Endege, Wilson O.			
APPLICANT: Gannavarapu, Manjula			
APPLICANT: Gorbacheva, Bella			
APPLICANT: Hoersch, Sebastian			
APPLICANT: Kamalakar, Shubhangi			
APPLICANT: Monsey, Angela M.			
APPLICANT: Glatz, Karen			
APPLICANT: Zhao, Xumei			
APPLICANT: Anderson, Dustin			
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND			
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
THERAPY OF PROSTATE CANCER			
FILE REFERENCE: MRI-044			
CURRENT APPLICATION NUMBER: US/10/205,823			

;
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-131

Query Match 85.5%; Score 1702.6; DB 14; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 240 AGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGAGTCATTCTACTCAGACCTGCTG 299
DB 899 AGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGAGTCATTCTACTCAGACCTGCTG 958
QY 300 ACTACTTTGCTCTGGGGGTGAAGTCCCTATCCACAGCGTTGGATCTTCTGGAGGTGTG 359
DB 959 ACTACTTTGCTCTGGGGGTGAAGTCCCTATCCAGATGGTTGGAACTTCTGGAGGTGTG 1018
QY 360 TCCAGCGTGAATATCCCTAAATCTGAATGGTGCAGAGAGACCTCTCACACCGATTACC 419
DB 1019 TCCAGCGTGAATATCCCTAAATCTGAATGGTGCAGAGAGACCTCTCTCACACCGATTACC 1078
QY 420 CAGCAATGAAATACGCTTATAGCATGAATGTCAGAGCGCTGTGCTTCCAGATTTC 479
DB 1079 CAGCAATGAAATACGCTTATAGCATGAATGTCAGAGCGCTGTGCTTCCAGATTTC 1138
QY 480 CTGTTCATCCAGTGTGATATATGATGCAAGAAAGCTCCCTAGAAAAATGGGTGCTCAG 539
DB 1139 CTGTTCATCCAGTGTGATATATGATGCAAGAAAGCTCCCTAGAAAAATGGGTGCTCAG 1198
QY 540 CACCACCAGATAGCAGCTGGAGAGAGTCTCAAAGTGTCTCAATGTTGACCTGCT 599
DB 1199 CACCACCAGATAGCAGCTGGAGAGAGTCTCAAAGTGTCTCAATGTTGACCTGCT 1258
QY 600 TTACTGAAACTTTTCTACACAAAAGTCAAGATGCATCCACTTACCAATGAAGTGA 659
DB 1259 TTACTGAAACTTTTCTACACAAAAGTCAAGATGCATCCACTTACCAATGAAGTGA 1318
QY 660 CGAGAAATTTACATGTGATAGTACCTCTCAGAGAGAGTGAACCAAGATATGTCA 719
DB 1319 CGAGAAATTTACATGTGATAGTACCTCTCAGAGAGAGTGAACCAAGATATGTCA 1378
QY 720 TTCTGGAGGTACCCGGAGCTCATGGGTGTTTGGTATTTGACCCCTCAGAGTGGAGCAG 779
DB 1379 TTCTGGAGGTACCCGGAGCTCATGGGTGTTTGGTATTTGACCCCTCAGAGTGGAGCAG 1438
QY 780 CTGTGTTCTAGAACTGTGAGAGCTTTTGAACACTGAAAAAGAAAGGTGTGAGACCTA 839
DB 1439 CTGTGTTCTAGAACTGTGAGAGCTTTTGAACACTGAAAAAGAAAGGTGTGAGACCTA 1498
QY 840 GAAGAACAAATTTGTTGTTGCAAGCTGGGATGCAGAAAGATTTGGTCTTCTGGTTCTACTG 899
DB 1499 GAAGAACAAATTTGTTGTTGCAAGCTGGGATGCAGAAAGATTTGGTCTTCTGGTTCTACTG 1558
QY 900 AGTGGCAGAGATAATTAAGACTCCTTCAAGAGCGTGGCGCTTATATTAAATGCTG 959
DB 1559 AGTGGCAGAGATAATTAAGACTCCTTCAAGAGCGTGGCGCTTATATTAAATGCTG 1618
QY 960 ACTCATCTATAGAGAAACTACACTGTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019
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DB 1619 ACTCATCTATAGAGAAACTACACTGTGAGAGTTGATTGTACACCGCTGATGTACAGCT 1678
QY 1020 TGGTATTAACACTTAACAAAAGAGCTGAAAAGCCCTGATGTAAGCTTTGAAGGCAAAATCTC 1079
DB 1679 TGGTACACAACTTAACAAAAGAGCTGAAAAGCCCTGATGTAAGCTTTGAAGGCAAAATCTC 1738
QY 1080 TTTATGAAGTTGGACTAAAAAAAGTCTTCCCGAGATTCAGTGGCATGCCAGATAA 1139
DB 1739 TTTATGAAGTTGGACTAAAAAAAGTCTTCCCGAGATTCAGTGGCATGCCAGATAA 1798
QY 1140 GCAAAATGGGATCTGGAATGATTTGAGGTGTTCTTCCACAGACTTGAATGCTTCAAG 1199
DB 1799 GCAAAATGGGATCTGGAATGATTTGAGGTGTTCTTCCACAGACTTGAATGCTTCAAG 1858
QY 1200 GCAGAGCGGTATTAATAAATTTGGAAACAAATTCACCGGCTATCCACTGTATC 1259
DB 1859 GCAGAGCGGTATTAATAAATTTGGAAACAAATTCACCGGCTATCCACTGTATC 1918
QY 1260 ACAGTGTCTATGAACATATGAGTGTGGTGAAGATTTTATGATCCAAATGTTAAATATC 1319
DB 1919 ACAGTGTCTATGAACATATGAGTGTGGTGAAGATTTTATGATCCAAATGTTAAATATC 1978
QY 1320 ACCTCACTGTGCCAGGTTGAGAGAGATGTTTGAAGTGAACCAATTCATATGTGC 1379
DB 1979 ACCTCACTGTGCCAGGTTGAGAGAGATGTTTGAAGTGAACCAATTCATATGTGC 2038
QY 1380 TCCCTTTGATGTCGAGATTATGCTGATTTTAAGAAATGTCGCAAAATGTACA 1439
DB 2039 TCCCTTTGATGTCGAGATTATGCTGATTTTAAGAAATGTCGCAAAATGTACA 2098
QY 1440 ATATTTCTATGAACATCCACAGAAATGAAGACATACAGTATTCATTTGATTCCTTT 1499
DB 2099 ATATTTCTATGAACATCCACAGAAATGAAGACATACAGTATTCATTTGATTCCTTT 2158
QY 1500 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAAAGTTCACGAGAGACTCCAGACT 1559
DB 2159 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAAAGTTCACGAGAGACTCCAGACT 2218
QY 1560 TTGCAAAAACCAACCAATTTGTTGAAGATGATGATCAACTGATTTCTGGAAA 1619
DB 2219 TTGCAAAAACCAACCAATTTGTTGAAGATGATGATGATCAACTGATTTCTGGAAA 2278
QY 1620 GAGCATTTATGATTCATTAAGGTTTACAGACAGACTTTTATAGCATGTCATATG 1679
DB 2279 GAGCATTTATGATTCATTAAGGTTTACAGACAGACTTTTATAGCATGTCATATG 2338
QY 1680 CTCACAGCCACACAACTATGACAGGGAGTCAATTTCCAGAAATTTATGATGCTGT 1739
DB 2339 CTCACAGCCACACAACTATGACAGGGAGTCAATTTCCAGAAATTTATGATGCTGT 2398
QY 1740 TTGATATTTGAACAAAGTGGACCTTCCAAAGGCTGGGGAGATGTAAGACAGATT 1799
DB 2399 TTGATATTTGAACAAAGTGGACCTTCCAAAGGCTGGGGAGATGTAAGACAGATT 2458
QY 1800 CTGTGAGCCTTACAGTGCAGAGCTTCAAGACTTTGAGTGAAGTAAAGAG 1859
DB 2459 ATGTGTGAGCCTTACAGTGCAGAGCTTCAAGACTTTGAGTGAAGTAAAGAG 2518
QY 1860 ATTCTTTAGAGACTCTGTATTTGAATTTGTGTGATGTCACTC--AAAGATATTAATG 1917
DB 2519 ATTCTTTAGAGACTCTGTATTTGAATTTGTGTGATGTCACTCAGAAAGATGTATG 2578
QY 1918 GTATATTTGAATTTTAAATTTGATATTTGAATTTGAATTTGAATTTGAATTTGAAT 1977
DB 2579 GTATATTTGAATTTTAAATTTGATATTTGAATTTGAATTTGAATTTGAATTTGAAT 2638
QY 1978 AAAAAAAAAAAAAA 1992
DB 2639 AAAAAAAAAAAAAA 2653

RESULT 7
US-09-978-295A-617

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; Sequence 617, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC11
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 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
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 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kijavrin, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James J.
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David A.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. McKey
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : TITLE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2630P1C27
 : CURRENT APPLICATION NUMBER: US/09/978,697
 : CURRENT FILING DATE: 2001-10-16
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2321 TTGATATTTGAAAGCAAAAGTGAACCTTCCAAAGCCTGGGAGATGTGAAGACAGATTT 2380
QY 1800 CTGTTGACGCTTTCACAGTGCAGGACGCTGCAAGACTTTGAGTAAAGTACCTTAAGAG 1859
2381 ATGTTGACGCTTTCACAGTGCAGGACGCTGCAAGACTTTGAGTAAAGTACCTTAAGAG 2440
QY 1860 ATTCCTTTGAGAGCTGTATGAAATTTGNGGTGATGTCACCT--AAAGATTAATAAGG 1917
2441 ATTTTGTGAGAGATCGTATGAAATTTGTGTGTATGTCACCTACAAAAAGATCGTAAAGG 2500
QY 1918 GATATTTGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATATTTATATATAA 1975
2501 GATATTTGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATATTTATATATAA 2558
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RESULT 9
US-09-978-192A-617
Sequence 617, Application US/09978192A
Patent No. US70020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 84.7%; Score 1687.2; DB 10; Length 2558;

Best Local Similarity 98.6%; Pred. No. 0; Mismatches 23; Indels 2; Gaps 1;

Matches 1713; Conservative 0;

QY 240 AGGTTAAATGCGCCAGCTGCGAGGGGCCAAAGAGTCATTCTCTACTGACCGCTGCTG 299
 DB 821 AGGTTAAATGCGCCAGCTGCGAGGGGCCAAAGAGTCATTCTCTACTGACCGCTGCTG 880
 QY 300 ACTACTTGTCTCTCTGCGGCTGAAGTCTTATCCAGACGCTTGAATCTTCTGAGGTGCTG 359
 DB 881 ACTACTTGTCTCTCTGCGGCTGAAGTCTTATCCAGACGCTTGAATCTTCTGAGGTGCTG 940
 QY 360 TCCAGCGTGAATATCTTAATCTGAATGCTCAGAGACCTCTCACCACGAGTTACC 419
 DB 941 TCCAGCGTGAATATCTTAAATCTGAATGCTCAGAGACCTCTCACCACGAGTTACC 1000
 QY 420 CAGCAATGATGCGCTTATAGCATGGAATGTCAGAGGCTGTGGCTTCCAAATATTC 479
 DB 1001 CAGCAATGATGCGCTTATAGCGTGAATGTCAGAGGCTGTGGCTTCCAAATATTC 1060
 QY 480 CTGTTCATCAGTTGATATATGATGACACAGAGCTCTAGAAAAATGGTGGCTGAC 539
 DB 1061 CTGTTCATCAGTTGATATGATGACACAGAGCTCTAGAAAAATGGTGGCTGAC 1120
 QY 540 CACCACCATAGACAGCTGAGAGGAGTCTCAAAGTGTCTCAATGTTGACCTGGCT 599
 DB 1121 CACCACCATAGACAGCTGAGAGGAGTCTCAAAGTGTCTCAATGTTGACCTGGCT 1180

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; PRIOR APPLICATION NUMBER: 60/085704
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; PRIOR APPLICATION NUMBER: 60/085697
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Query Match	84.7%	Score 1687.2;	DB 10;	Length 2558;
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OY	240	AGGTTAAATAATGCCACCTGGACGAGGGCCAAAGAGATCATTCCTACTCTACAGACCTCTG	239
Db	821	AGGTTAAATAATGCCACCTGGACGAGGGCCAAAGAGATCATTCCTACTCTACAGACCTCTG	880
OY	300	ACTACTTTCCTCTCGGGGTGAAGTCTATCCAGACGGTTGGAAATCTTCTCGTAGAGTGTG	359
Db	881	ACTACTTTCCTCTCGGGGTGAAGTCTATCCAGACGGTTGGAAATCTTCTCGTAGAGTGTG	940
OY	360	TTCCAGCGTGGAAATATCTCTAAATCTGAATGTGTGCAGAGACCCCTCTACACACAGTTACC	419
Db	941	TTCCAGCGTGGAAATATCTCTAAATCTGAATGTGTGCAGAGACCCCTCTACACACAGTTACC	1000
OY	420	CAGCAAAATGATATAGCGCTATATAGGATGGAATTCAGAGAGCGCTTGAGCTTCCAGATATTC	479
Db	1001	CAGCAAAATGATATAGCGCTATATAGGATGGAATTCAGAGAGCGCTTGAGCTTCCAGATATTC	1060
OY	480	CTGTTTCATCCAGTTGGATATATGATGACAGAAAGCTCTAGAAAAAATGGGTGGCTAG	539
Db	1061	CTGTTTCATCCAGTTGGATATATGATGACAGAAAGCTCTAGAAAAAATGGGTGGCTAG	1120
OY	540	CACCAACCGATATGACGCTGAGAGAGGAATCTCAAAAGTGTCCTACAAATGGTAGACCTGGCT	599
Db	1121	CACCAACCGATATGACGCTGAGAGAGGAATCTCAAAAGTGTCCTACAAATGGTAGACCTGGCT	1180
OY	600	TTACTGGAACCTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA	659
Db	1181	TTACTGGAACCTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA	1240
OY	660	CGAGAAATTTACAAATGTGATAGTACTCTCAGAGGACAGTGGAAACACAGACATATGTCA	719
Db	1241	CGAGAAATTTACAAATGTGATAGTACTCTCAGAGGACAGTGGAAACACAGACATATGTCA	1300
OY	720	TTCTGGGAGGTCACCGGGACATGAGGTTGTTGGTGATTTGACCTTCAGAGTGGAGAG	779
Db	1301	TTCTGGGAGGTCACCGGGACATGAGGTTGTTGGTGATTTGACCTTCAGAGTGGAGAG	1360
OY	780	CTGTGTTTCATGAAACCTGTGAGAGACTTTTGGAACTGTAAAAAGGAAGGTGAGACCTTA	839
Db	1361	CTGTGTTTCATGAAACCTGTGAGAGACTTTTGGAACTGTAAAAAGGAAGGTGAGACCTTA	1420
OY	840	GAAGAACAATTTTCTTTCGAAGCTGGGATGACAGAAATTTTGTCCTTCTGTTCTACTG	899
Db	1421	GAAGAACAATTTTCTTTCGAAGCTGGGATGACAGAAATTTTGTCCTTCTGTTCTACTG	1480
OY	900	AGTGGGACAGAGATATATTCAGACTTCCTTCAAGAGCGTGGGTGCTTATATTAATGCTG	959
Db	1481	AGTGGGACAGAGAGATATTCAGACTTCCTTCAAGAGCGTGGGTGCTTATATTAATGCTG	1540
OY	960	ACTCATCTATAGAAGGAACCTACATCTGAGAGTGTGATTTGTACACACATGATGTACACT	1019
Db	1541	ACTCATCTATAGAAGGAACCTACATCTGAGAGTGTGATTTGTACACACCGCTGATGTACACT	1600
OY	1020	TGGTATACACCTTAACAAAGAGCTGAAGAGGCCCTGATGAAGGCTTTTGAAGGCAAAATCTC	1079
Db	1601	TGGTATACACCTTAACAAAGAGCTGAAGAGGCCCTGATGAAGGCTTTTGAAGGCAAAATCTC	1660
OY	1080	TTTATGAAGATTGGACTTAAAAAAGTCTTCCCAAGATTAGTGGCATGCCAGAGATTA	1139
Db	1661	TTTATGAAGATTGGACTTAAAAAAGTCTTCCCAAGATTAGTGGCATGCCAGAGATTA	1720
OY	1140	GCAAAATGGGATCTGGAAATGAATTTTGAAGTGTTCTTCCAAACGACTTGGAAATGGCTCAG	1199
Db	1721	GCAAAATGGGATCTGGAAATGAATTTTGAAGTGTTCTTCCAAACGACTTGGAAATGGCTCAG	1780

QY	1200	GCACAGCAGCGTATCTCAAAATAATTGGGAAAACAAACAAATTCAGGGGCTATCCACTGTATC	1259
Db	1781	GCACAGCAGCGTATCTCAAAATAATTGGGAAAACAAACAAATTCAGGGGCTATCCACTGTATC	1840
QY	1260	ACAGTGTCTATGAAACAATCATGAGTTGGGTGGAAAAATTATATGATCCAAATGTTTAAATATC	1319
Db	1841	ACAGTGTCTATGAAACAATCATGAGTTGGGTGGAAAAATTATATGATCCAAATGTTTAAATATC	1900
QY	1320	ACCTCACTGTGGCCCGAGGTTGAGAGAGGATGGTGTGGAGCTTAGACCTTAGCCAAATTCATAGTGC	1379
Db	1901	ACCTCACTGTGGCCCGAGGTTGAGAGAGGATGGTGTGGAGCTTAGACCTTAGCCAAATTCATAGTGC	1960
QY	1380	TCCTCTTTTGATGTGCGAGTATATGCTGTAGTTTAAAGAAAGTATGCTGACAAAAATCTACA	1439
Db	1961	TCCTCTTTTGATGTGCGAGTATATGCTGTAGTTTAAAGAAAGTATGCTGACAAAAATCTACA	2020
QY	1440	ATATTTCTATGAACAATCCACAGGAAATGAAAGACATACATTTATCATTTTGATTCACCTT	1499
Db	2021	GTATTTCTATGAACAATCCACAGGAAATGAAAGACATACATTTATCATTTTGATTCACCTT	2080
QY	1500	TTTCTGCGATAAAAAATTTTACAGAAATGCTTCCAAAGTTCCAGCGAAGACCTCAGACT	1559
Db	2081	TTTCTGCGATAAAAAATTTTACAGAAATGCTTCCAAAGTTCCAGCGAAGACCTCAGACT	2140
QY	1580	TTGCAAAAGCAACCCCAATTTGTTAAGAAATGATGAATGATCACTGATGTTTCTGAAA	1619
Db	2141	TTGCAAAAGCAACCCCAATTTGTTAAGAAATGATGAATGATCACTGATGTTTCTGAAA	2200
QY	1620	GAGCATTTATTTGATTCATTAGAGGTTTACCAGACAGACCTTTTATAGCATGCTATCTATG	1679
Db	2201	GAGCATTTATTTGATTCATTAGAGGTTTACCAGACAGACCTTTTATAGCATGCTATCTATG	2260
QY	1680	CTCCACAGCAGCCACACAAAGTATGCGAGGGAGTCAATTCACAGAAATTTATCATGCTCTGT	1739
Db	2261	CTCCACAGCAGCCACACAAAGTATGCGAGGGAGTCAATTCACAGAAATTTATCATGCTCTGT	2320
QY	1740	TTGATATTGAAAGCAAAAGTGGAGCCCTTCCAAAGCCTGGGAGAGTGTGAAGACAGATTT	1799
Db	2321	TTGATATTGAAAGCAAAAGTGGAGCCCTTCCAAAGCCTGGGAGAGTGTGAAGACAGATTT	2380
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QY	1860	ATTCCTTTAGAGACTCTGATTTGAATTTGTGTGATATGTCATCTC--AAAGATTAATTAAGG	1917
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QY	1918	GTATATTGATTAATTTTAAATTTGGTATATTGAAATAAGTGAATTTATTAATTA	1975
Db	2501	GTATATTGATTAATTTTAAATTTGGTATATTGAAATAAGTGAATTTATTAATTA	2558
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: Publication No. US20030004102A1			
: GENERAL INFORMATION:			
: APPLICANT: Ashkenazi, Avi			
: APPLICANT: Baker Kevin P.			
: APPLICANT: Botstein, David			
: APPLICANT: Desnoyers, Luc			
: APPLICANT: Eaton, Dan			
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 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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22 PRIOR APPLICATION NUMBER: 60/085582
23 PRIOR FILING DATE: 1998-05-15
24 PRIOR APPLICATION NUMBER: 60/085700
25 PRIOR FILING DATE: 1998-05-15
26 PRIOR APPLICATION NUMBER: 60/085689
27 PRIOR FILING DATE: 1998-05-15
28 PRIOR APPLICATION NUMBER: 60/085579
29 PRIOR FILING DATE: 1998-05-15
30 PRIOR APPLICATION NUMBER: 60/085580
31 PRIOR FILING DATE: 1998-05-15
32 PRIOR APPLICATION NUMBER: 60/085573
33 PRIOR FILING DATE: 1998-05-15
34 PRIOR APPLICATION NUMBER: 60/085704
35 PRIOR FILING DATE: 1998-05-15
36 PRIOR APPLICATION NUMBER: 60/085697

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Query Match	84.7%;	Score 1687.2;	DB 11;	Length 2558;
Best Local Similarity	98.6%;	Pred. No. 0;		
Matches 1713;	Conservative	0;	Mismatches 23;	Indels 2;
				Gaps 1;
QY	240	AGGTTAAAGATGCCAGGCTGGCAGGGGGCAAGGAGTATCTCTACTCAGACCCGTGTG	299	
Db	821	AGGTTAAAGATGCCAGGCTGGCAGGGGGCAAGGAGTATCTCTACTCAGACCCGTGTG	880	
QY	300	ACTACTTGTGCTCTGGGGTGAAGTCTTATCCAGACGGTTGGAATCTTCTGGAGGTGTG	359	
Db	881	ACTACTTGTGCTCTGGGGTGAAGTCTTATCCAGACGGTTGGAATCTTCTGGAGGTGTG	940	
QY	360	TCCAGCGCTGGAAATATCTTAATCTGAAATGTGTGAGGAGACCCCTCTACACAGGTATAC	419	
Db	941	TCCAGCGCTGGAAATATCTTAATCTGAAATGTGTGAGGAGACCCCTCTACACAGGTATAC	1000	
QY	420	CAGCAAAATGAATACGCTTATAGGCAATGAGATTCGAGAGCTGTGGTTCCTCCAAATATTC	479	
Db	1001	CAGCAAAATGAATATGCTTATATAGGCTGGAAATTCGAGAGCTGTGGTTCCTCCAAATATTC	1060	
QY	480	CTGTTCATCCAGTTGGATATCTATGATGTCACAGAACTCTTAGAAAAATTTGGTGGCTTAG	539	
Db	1061	CTGTTCATCCAGTTGGATATCTATGATGTCACAGAACTCTTAGAAAAATTTGGTGGCTTAG	1120	
QY	540	CACCAACCGATATGAGCGTGGAGAGAACTCCAAAGTGTCTTACAAATTTGGACCTGGCT	599	
Db	1121	CACCAACCGATATGAGCGTGGAGAGAACTCTCAAAGTGTCTTACAAATTTGGACCTGGCT	1180	
QY	600	TTACTGGAACCTTTTCTACAAAAAAGTCAAGATGCACATCCACATCTTACCAATGAAGTGA	659	
Db	1181	TTACTGGAACCTTTTCTACAAAAAAGTCAAGATGCACATCCACATCTTACCAATGAAGTGA	1240	
QY	660	CGAGAAATTTACAAATGTGATAGTACTCTCAGAGAGCAGTGGAAACCAAGATATGTCA	719	
Db	1241	CGAGAAATTTACAAATGTGATAGTACTCTCAGAGAGCAGTGGAAACCAAGATATGTCA	1300	

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Db      2381 ATGTCGACGCTTCACAGTCAGGACAGCTTGAGTGAAGTGAAGAGG 2440
QY      1860 ATTCTTTAGAGACCTCTATTTGAATTTGTGTGATATCTC- -AAGATATATATGG 1917
Db      2441 ATTTTTTAGAATCCGATTTGAATTTGTGTGTCTCCTACGAAAGATCGTATG 2500
QY      1918 GTATATTGATTAATTTTAAATTTGTATTTTGAATTAATATATATA 1975
Db      2501 GTATATTGATTAATTTTAAATTTGTATTTTGAATTAATATATATA 2558

RESULT 12
US-09-978-608A-617
: Sequence 617, Application US/09978608A
: Publication No. US20030045462A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Flivaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2630PIC22
: CURRENT APPLICATION NUMBER: US/09/978, 608A
: CURRENT FILING DATE: 2001-10-16
: NUMBER OF SEQ ID NOS: 624
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 617
: LENGTH: 2558
: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-978-608A-617

Query Match      84.7%; Score 1687.2; DB 11: Length 2558;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

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QY      420 CAGCAATGATAACGCTTATAGCATGAATTCGAGAGGCTGTGTCTTCCAAATATTC 479
Db      1001 CAGCAATGATAATATGCTTATAGGCGTGAATTCGAGAGGCTGTGTCTTCCAAATATTC 1060
QY      480 CTGTTTCATCCAGTTGGATTAATGATGTCACAGAGCTCTTGAAGAAATGGGTGGTCAG 539
Db      1061 CTGTTTCATCCAAATGGATTAATGATGTCACAGAGCTCTTGAAGAAATGGGTGGTCAG 1120
QY      540 CACCACAGATAGCAGCTGGAGAGAAAGTCTCAAGTGTCTTCAATGTTGGACCTGGCT 599
Db      1121 CACCACAGATAGCAGCTGGAGAGAAAGTCTCAAGTGTCTTCAATGTTGGACCTGGCT 1180
QY      600 TTACTGAAACTTTTTCACACAAAGATGATGATCCATCCATCCAAATGAAGTGA 659
Db      1181 TTACTGAAACTTTTTCACACAAAGATGATGATCCATCCATCCAAATGAAGTGA 1240
QY      660 CGAGAAATTTCAATGTATAGTACTCTCAGAGAGAGCAGTGAACAGAGATATGTCA 719
Db      1241 CGAGAAATTTCAATGTATAGTACTCTCAGAGAGAGCAGTGAACAGAGATATGTCA 1300
QY      720 TTCTGGAGGTCACCGGAGCTCATGGGTGTTTGTGTATTTGACCTCAGAGTGGACAG 779
Db      1301 TTCTGGAGGTCACCGGAGCTCATGGGTGTTTGTGTATTTGACCTCAGAGTGGACAG 1360
QY      780 CTGTTTTCATGAACCTGTAGAGAGCTTTGAAACACTGAAGAAAGGAGGTGGAGACTA 839
Db      1361 CTGTTTTCATGAACCTGTAGAGAGCTTTGAAACACTGAAGAAAGGAGGTGGAGACTA 1420
QY      840 GAAGAAATTTTGTTCGCAAGCTGGAGTGCAGAGAAATTTGTCTTGTCTTACTG 899
Db      1421 GAAGAAATTTTGTTCGCAAGCTGGAGTGCAGAGAAATTTGTCTTGTCTTACTG 1480
QY      900 AGTGGCAGAGGATTAATCAAGCTCTTCAAGAGCTGGCGTGTATATTAATGCTG 959
Db      1481 AGTGGCAGAGGATTAATCAAGCTCTTCAAGAGCTGGCGTGTATATTAATGCTG 1540
QY      960 ACTCATCTATAGAAGAACTATACCTGTAGAGTGTATTAACCACTGATGTACAGCT 1019
Db      1541 ACTCATCTATAGAAGAACTATACCTGTAGAGTGTATTAACCACTGATGTACAGCT 1600
QY      1020 TGGTATTAACAACCTAACAAGAGCTGAAAGCCCTGTATGAAGCTTTGAAGCAATCTC 1079
Db      1601 TGGTATTAACAACCTAACAAGAGCTGAAAGCCCTGTATGAAGCTTTGAAGCAATCTC 1660
QY      1080 TTATATGAATTTGGACTTAAAAAGTCTTCCCAAGTTCAGTGGATGCCCAAGATA 1139
Db      1661 TTATATGAATTTGGACTTAAAAAGTCTTCCCAAGTTCAGTGGATGCCCAAGATA 1720
QY      1140 GCAAAATTTGGAGTGTGAATGATTTTGGAGTGTCTTCCAAAGCTTGAATTCCTGAG 1199
Db      1721 GCAAAATTTGGAGTGTGAATGATTTTGGAGTGTCTTCCAAAGCTTGAATTCCTGAG 1780
QY      1200 GCAGAGCAGGATTAATTAATAATTTGGGAAACAAACAAATTCACGGCTATCCACTGTATC 1259
Db      1781 GCAGAGCAGGATTAATTAATAATTTGGGAAACAAACAAATTCACGGCTATCCACTGTATC 1840
QY      1260 ACAAGTCTATGAACATATAGAGTGTGGAAGAAATTTATGATCCAAATTTTAAATATC 1319
Db      1841 ACAAGTCTATGAACATATAGAGTGTGGAAGAAATTTATGATCCAAATTTTAAATATC 1900
QY      1320 ACCTCACTGTGGCCAGGTCGAGAGAGAGTGTGTTTGAAGTGAAGCAATTCATAGTGC 1379
Db      1901 ACCTCACTGTGGCCAGGTCGAGAGAGAGTGTGTTTGAAGTGAAGCAATTCATAGTGC 1960
QY      1380 TCCCTTTTGAATGTGAGATTAATGCTGATTTTGAAGAAATGCTGACAAATCTACA 1439
Db      1961 TCCCTTTTGAATGTGAGATTAATGCTGATTTTGAAGAAATGCTGACAAATCTACA 2020
QY      1440 ATATTTCTATGAACATCCACAGAGAAATGAAGCATATCAATTTATATTTGATTCACCTT 1499
Db      2021 ATATTTCTATGAACATCCACAGAGAAATGAAGCATATCAATTTATATTTGATTCACCTT 2080
QY      1500 TTCTGTGAGTAAATAATTTTACAGAAATTCCTTCCAAAGTTCAGAGAGACTCCAGACT 1559

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Db      2081  TTTCTGAGTAAAGAAATTTTACAGAAATTTGCTTCAAGTTCAGAGAGAGCTCCAGAGCT 2140
OY      1560  TTGACAAAGACCAACCAATATTTGTAAGAAATGATGAATGATCACTCATGTTCTGGAAA 1619
Db      2141  TTGCAAAAAGACCAACCAATAGTATTAAGAAATGATGAATGATCACTCATGTTCTGGAAA 2200
OY      1620  GAGCAATTTATTTGATTCATTTAGGGTTTACCAGACAGACCTTTTATAGCAGTCTATG 1679
Db      2201  GAGCAATTTATTTGATTCATTTAGGGTTTACCAGACAGACCTTTTATAGCAGTCTATG 2260
OY      1680  CTCCAAGCAGCCAAACAAAGATATGACAGGGGAGTCATTTCCCGAATTTATATCTCTGT 1739
Db      2261  CTCCAAGCAGCCAAACAAAGATATGACAGGGGAGTCATTTCCCGAATTTATATCTCTGT 2320
OY      1740  TTGATATTTGAAGAAAGTGGACCTTCCAGAGCCTGGGAGAGATGTGAAGACAGATTT 1799
Db      2321  TTGATATTTGAAGAAAGTGGACCTTCCAGAGCCTGGGAGAGATGTGAAGACAGATTT 2380
OY      1800  CTGTTGACGCTTACAGAGTGCAGGACGCTGCAGAGACTTTGATGAAAGTACCTTAAGAG 1859
Db      2381  ATGTTGACGCTTACAGAGTGCAGGACGCTGCAGAGACTTTGATGAAAGTACCTTAAGAG 2440
OY      1860  ATTCTTGAAGACCTGATGATGAATTTGTGTATGTCACCTC--AAAGAAATTAATG 1917
Db      2441  ATTTTTTGAAGAAATCCGATTTGAATTTGTGTATGTCACCTCAGAAAGAAATCGTAATG 2500
OY      1918  GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATTTATTAATTA 1975
Db      2501  GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATTTATTAATTA 2558
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RESULT 13
US-09-978-585A-617

Sequence 617, Application US/09978585A

Publication No. US20030049633A1

GENERAL INFORMATION:

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: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630pic15
: CURRENT APPLICATION NUMBER: US/09/978,585A
: NUMBER OF SEQ ID NOS: 624
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 617
: LENGTH: 2558
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: TYPE: DNA
: ORGANISM: Homo Sapien
: US-09-978-585A-617
Query Match      84.7%; Score 1687.2; DB 11; Length 2558;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

OY      240  AGGTTAAATAATGCCAGCTGGCAGGGCCAAAGAGTCATCTTCTACTCAGACCTCTCTG 299
Db      821  AGGTTAAATAATGCCAGCTGGCAGGGCCAAAGAGTCATCTTCTACTCAGACCTCTCTG 880
OY      300  ACTACTTTCCTCCGGGGTGAAGTCATATCCAGAGGGTTGGAAATCTTCTGAGAGTGTG 359
Db      881  ACTACTTTCCTCCGGGGTGAAGTCATATCCAGAGGGTTGGAAATCTTCTGAGAGTGTG 940
OY      360  TCCAGCGTGAATAATCTTAATCTGAATGTGACAGAGACCTCTCACACACAGTTACC 419
Db      941  TCCAGCGTGAATAATCTTAATCTGAATGTGACAGAGACCTCTCACACACAGTTACC 1000
OY      420  CAGCAATGAATACGCTTATAGCATGGAATTCGAGAGGCTGTGTCTTCCAAAGTATTC 479
Db      1001  CAGCAATGAATATGATATGAGCGTGAATTCGAGAGGCTGTGTCTTCCAAAGTATTC 1060
OY      480  CTGTTCAATCCAGTTGATATGATGACAGAGAGCTCCCTGAAATAATGGGTGGCTCAG 539
Db      1061  CTGTTCAATCCAGTTGATATGATGACAGAGAGCTCCCTGAAATAATGGGTGGCTCAG 1120
OY      540  CACCACAGATAGCAGCTGAGAGAAAGTCTCAAGTGTCTCTACAAATGTTGACCTGGCT 599
Db      1121  CACCACAGATAGCAGCTGAGAGAAAGTCTCAAGTGTCTCTACAAATGTTGACCTGGCT 1180
OY      600  TTACTGGAATTTTCTACACAAAAGTCAAGATGACATCTCCATCAATGAATGA 659
Db      1181  TTACTGGAATTTTCTACACAAAAGTCAAGATGACATCTCCATCAATGAATGA 1240
OY      660  CGAGAAATTTCAATGTGATAGTACTCTCAGAGAGCAGTGAACACAGACATATGTCA 719
Db      1241  CGAGAAATTTCAATGTGATAGTACTCTCAGAGAGCAGTGAACACAGACATATGTCA 1300
OY      720  TTCTGGAGAGTCCACGGGACTCATGGGTGTTGGTGTATTTGACCTCAGAGTGGACAG 779
Db      1301  TTCTGGAGAGTCCACGGGACTCATGGGTGTTGGTGTATTTGACCTCAGAGTGGACAG 1360
OY      780  CTGTTGTTCAATGAATCTGTGAGAGCTTTGGAACACATGAAAAGAAAGCGTGGAGACCTA 839
Db      1361  CTGTTGTTCAATGAATCTGTGAGAGCTTTGGAACACATGAAAAGAAAGCGTGGAGACCTA 1420
OY      840  GAAGAAATTTTGTGTTGCAAGCTGGAGTGCAGAAAGATTTGTCTTGTGTTCTACTG 899
Db      1421  GAAGAAATTTTGTGTTGCAAGCTGGAGTGCAGAAAGATTTGTCTTGTGTTCTACTG 1480
OY      900  AGTGGGACAGAGATTAATCAAGACTCTTCAAGAGCTGGCGTGGCTTATTTAATGCTG 959
Db      1481  AGTGGGACAGAGATTAATCAAGACTCTTCAAGAGCTGGCGTGGCTTATTTAATGCTG 1540
OY      960  ACTCATCTATGAAAGAAACATCACTCTGAGAGTTGATTTACACCACTGATGACACT 1019
Db      1541  ACTCATCTATGAAAGAAACATCACTCTGAGAGTTGATTTACACCACTGATGACACT 1600
OY      1020  TGGTATACACCTTAACAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAAAGCAATCTC 1079
Db      1601  TGGTATACACCTTAACAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAAAGCAATCTC 1660
OY      1080  TTTATGAAGTGTGACATAAAAAAGCTCTCCCGAGCTTACAGTTCAGTGCACAGATTA 1139
Db      1661  TTTATGAAGTGTGACATAAAAAAGCTCTCCCGAGCTTACAGTTCAGTGCACAGATTA 1720
OY      1140  GCAATTTGGATCTGGAATATGTTTGAAGGTCTTCTTCCACAGACTTGAATGCTTACG 1199
Db      1721  GCAATTTGGATCTGGAATATGTTTGAAGGTCTTCTTCCACAGACTTGAATGCTTACG 1780
OY      1200  GCAGAGCAGCGTATCTAATAAATTTGGAACAAACAAATTCAGCGGTATCCACTGATTC 1259
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|||||
Db 1781 GCAGAGCAGCGTATCTAAAAATGGCAACAAACAAATTCAGGGCTATCCACTGATC 1840
QY 1260 ACAGTCTCTATGAAACATATGAGTGTGTGAAAAAGTTTATGATCCATGTTTAAATATC 1319
Db 1841 ACATGCTCTATGAAACATATGAGTGTGTGAAAAAGTTTATGATCCATGTTTAAATATC 1900
QY 1320 ACCTCACTGTGGCCAGGTTGCGAGAGAGATGGTGTGAGTCCATGAGCAATTCATAGTGC 1379
Db 1901 ACCCTCACTGTGGCCAGGTTGCGAGAGAGATGGTGTGAGTCCATGAGCAATTCATAGTGC 1960
QY 1380 TCCCTTTGATGTGCGAGTATGCTGTAGCTTTTAAAGAAATGCTGACAAAATCTACA 1439
Db 1961 TCCCTTTGATGTGCGAGTATGCTGTAGCTTTTAAAGAAATGCTGACAAAATCTACA 2020
QY 1440 ATATTTCTATGAAACATCCACAGAAATGAAGACATACATTTATCTATTTGATTCACCTT 1499
Db 2021 GTATTTCTATGAAACATCCACAGAAATGAAGACATACATTTATCTATTTGATTCACCTT 2080
QY 1500 TTTCTGAGTAAAAAATTTTACAGAAATGCTTCCAGTCCAGAGAGACTCCAGACT 1559
Db 2081 TTTCTGAGTAAAAAATTTTACAGAAATGCTTCCAGTCCAGAGAGACTCCAGACT 2140
QY 1560 TTGACAAAAGCAACCAATATGTTTAAAGAAATGATGATGATCAACTCATGTTCTGAAA 1619
Db 2141 TTGACAAAAGCAACCAATATGTTTAAAGAAATGATGATGATCAACTCATGTTCTGAAA 2200
QY 1620 GACCATTTATGATTCATTTAGGGTTACACAGAGACTTTTATAGCATGATCATGATG 1679
Db 2201 GACCATTTATGATTCATTTAGGGTTACACAGAGACTTTTATAGCATGATCATGATG 2260
QY 1680 CTCGAAGCAGCCACCAACATATGTCAGAGGAGTCAATCCAGAAATTTATGATGCTGT 1739
Db 2261 CTCGAAGCAGCCACCAACATATGTCAGAGGAGTCAATCCAGAAATTTATGATGCTGT 2320
QY 1740 TTGATATGAAACAAAGTGAGCCCTTCCAAGGCTGGGGAGATGTGAAGACAGAGATT 1799
Db 2321 TTGATATGAAACAAAGTGAGCCCTTCCAAGGCTGGGGAGATGTGAAGACAGAGATT 2380
QY 1800 CTGTTGAGCCCTTCACAGTCCAGGAGGCTCCACAGACTTTGATGAGAGTACCTAAGAG 1859
Db 2381 ATGTTGAGCCCTTCACAGTCCAGGAGGCTCCACAGACTTTGATGAGAGTACCTAAGAG 2440
QY 1860 ATTTCTTAGAGACTCTGATTTGATTTGTGTGATGTCACTC--AAAGAAATATATG 1917
Db 2441 ATTTCTTAGAGACTCTGATTTGATTTGTGTGATGTCACTCAGAAAGAAATGATATG 2500
QY 1918 GTATATTTGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATATATATATA 1975
Db 2501 GTATATTTGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATATATATATA 2558

RESULT 14

US-09-978-191A-617
; Sequence 617, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J

APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
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Query Match 84.7%; Score 1687.2; DB 11; Length 2558;
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Query Match 84.7%; Score 1687.2; DB 11; Length 2558;
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 587654.

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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SUMMARIES

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ALIGNMENTS

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; Sequence 944, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
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; LENGTH: 750
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; ORGANISM: Homo sapiens
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Query Match 98.2%; Score 2288; DB 9; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
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: Patent No. US20020156006A1
: GENERAL INFORMATION:
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: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tomas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630P1C11
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085697
Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGSSAPDDSSMRGSLKYSVNWGPGFTGNFSTQKVKMHISTNEVTRIVNYIGTLRGAVEP 60
DB 309 MGSSAPDDSSMRGSLKYPVWVGPGFTGNFSTQKVKMHISTNEVTRIVNYIGTLRGAVEP 368
QY 61 DRYVILGHRDSSVFGGIDPQGAAYVHETVRSFGTLKKEGMPRRRTILFASWDAEEFGL 120
DB 369 DRYVILGHRDSSVFGGIDPQGAAYVHETVRSFGTLKKEGMPRRRTILFASWDAEEFGL 428
QY 121 LGSTEWAEONSRLLOEGRVAVINADSSIEGNTLRDCCPLMTSLVHNLTKEKSPDEGP 180
DB 429 LGSTEWAEONSRLLOEGRVAVINADSSIEGNTLRDCCPLMTSLVHNLTKEKSPDEGP 488
QY 181 EGSLSYESWTKKSPSPESFGMPRIKSGNDPEVEFFORLGISGRARYTKMNETKFSG 240
DB 489 EGSLSYESWTKKSPSPESFGMPRIKSGNDPEVEFFORLGISGRARYTKMNETKFSG 548
QY 241 YPLHSHYETTELVEKRYDPMFKYHLTVACVRCGMVPELANSIVLPDCCRDAVAVLRKTA 300
DB 549 YPLHSHYETTELVEKRYDPMFKYHLTVACVRCGMVPELANSIVLPDCCRDAVAVLRKTA 608
QY 301 DKTYNISMKHPQEMKTYSLSPDLSFAVKNFTETIAKFSRLODPKSNPILRMNNDL 360
DB 609 DKTYNISMKHPQEMKTYSLSPDLSFAVKNFTETIAKFSRLODPKSNPILRMNNDL 668
QY 361 MFLERAFIDPLGIDPRPEFYHVIYAPSSHNKRYAGESFPGIYDALFDIESKVDKAMGV 420
DB 669 MFLERAFIDPLGIDPRPEFYHVIYAPSSHNKRYAGESFPGIYDALFDIESKVDKAMGV 728
QY 421 KROIYVAFTVQAAETLSEVA 442
DB 729 KROIYVAFTVQAAETLSEVA 750
RESULT 3
US-09-978-697-618
Sequence 618, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoul, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

FILE REFERENCE: P2630PLC27
CURRENT APPLICATION NUMBER: US/09/978.697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

Query Match      98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7, 3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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DB 369 DRVYILGHRDMSVFGIPDQGAAYVHETVRSFGLTKKEGMPRTIIFASWDAEFGI 428
QY 121 LGSTWAEEDNSRLDGRVAYINADSSIEGNTTLRVDCPTLMYSLVNLTKELKSPDEG 180
DB 429 LGSTWAEEDNSRLDGRVAYINADSSIEGNTTLRVDCPTLMYSLVNLTKELKSPDEG 488
QY 181 EKSSTYESTWTKSPSEFSGMPRIKSLGSGNDPEVFOGLGASGARTTKWETKESG 240
DB 489 EKSSTYESTWTKSPSEFSGMPRIKSLGSGNDPEVFOGLGASGARTTKWETKESG 548
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QY 301 DKTYINSMKHPOEMKTYSLSPDSLSAVKNFTEIASKFSERLQDPEKSNPILLRMNDOL 360
DB 609 DKTYINSMKHPOEMKTYSLSPDSLSAVKNFTEIASKFSERLQDPEKSNPILLRMNDOL 668
QY 361 MFLERAFIDPLGIDPRPFRRHYIYAPSSHNKKAAGESFBIYDALPDIKSKVDSKAWGV 420
DB 669 MFLERAFIDPLGIDPRPFRRHYIYAPSSHNKKAAGESFBIYDALPDIKSKVDSKAWGV 728
QY 421 KROIIVAAFTVOAAETLSEVA 442
DB 729 KROIIVAAFTVOAAETLSEVA 750

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APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978, 192A
CURRENT FILING DATE: 2001-10-15
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RESULT 4
US-09-978-192A-618
Sequence 618, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman

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PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSWRGSLKYSYVNGPGFTGNFSTOKVKMHIHSTNEVTRITYNYIGTLRGAVEP 60
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QY 61 DRYVILGHRDSWVFGGIDPOSGAAVYHEIVRSFGTLKKEGMRPRRTIILASMDAEFGL 120
DB 369 DRYVILGHRDSWVFGGIDPOSGAAVYHEIVRSFGTLKKEGMRPRRTIILASMDAEFGL 428
QY 121 LGSTEMAEDNSRLLOEGVAVYINADSSIEGNYTLRVCTPLMYSLVYVNLTKELKSPDEGF 180
DB 429 LGSTEMAEDNSRLLOEGVAVYINADSSIEGNYTLRVCTPLMYSLVYVNLTKELKSPDEGF 488
QY 181 EGKSLYESWTKRSPSPFGMPRIKSLGSGNDFEVFFQRLGASGRARYTKMNETNFKFSG 240
DB 489 EGKSLYESWTKRSPSPFGMPRIKSLGSGNDFEVFFQRLGASGRARYTKMNETNFKFSG 548
QY 241 YPLVHSYETVELYERKYDDPFKHLTVAOYRGGMVETELANSIYLPDPCDXYAVVLRKYA 300
DB 549 YPLVHSYETVELYERKYDDPFKHLTVAOYRGGMVETELANSIYLPDPCDXYAVVLRKYA 608
QY 301 DKYINISMKHPQEKKTYSLSFDSLSFAVKNFTELASFESRLODFDKSNPILLRMMNDOL 360
DB 609 DKYISIMKHPQEKKTYSLSFDSLSFAVKNFTELASFESRLODFDKSNPILLRMMNDOL 668
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Db 669 MLELRATIDPLGIDRPFYRIVAPSSHNKYGESFPGIADLFJESKVDPSKAMGEV 728
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Db 729 KROIYVAFTVOAAEFTLSEVA 750

RESULT 5.
US-09-999-832A-618
Sequence 618, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 1 MGSAAPPDSSWRGSLKVSXVNGPFTGNFSTOKVKMHISTNEVTRIIYVIGTLRGAVEP 60
DB 309 MGSAAPPDSSWRGSLKVSXVNGPFTGNFSTOKVKMHISTNEVTRIIYVIGTLRGAVEP 368

OY 61 DRYVILGGHRDSWVFGIDPQSGAAVVEHVRSFGLTKEGMRPRRTILFASMDAEEFGL 120
DB 369 DRYVILGGHRDSWVFGIDPQSGAAVVEHVRSFGLTKEGMRPRRTILFASMDAEEFGL 428
OY 121 LGSTEWADNSRLLOERGVAVINADSSIEGVYTLRVDCPTPLMYSLVYNLTETELSPDEGF 180
DB 429 LGSTEWADNSRLLOERGVAVINADSSIEGVYTLRVDCPTPLMYSLVYNLTETELSPDEGF 488
OY 181 ECKSLYESWTKKSPSPFSGMPRIKSLGSGNDPEVFQRLIASGRARYTNWETNKFSG 240
DB 489 ECKSLYESWTKKSPSPFSGMPRIKSLGSGNDPEVFQRLIASGRARYTNWETNKFSG 548
OY 241 YPLHVSVEYETELVEKEFYDPMFKYHLFVAQYRGVAFELANSIVLPEDCRDYAVVLKRYA 300
DB 549 YPLHVSVEYETELVEKEFYDPMFKYHLFVAQYRGVAFELANSIVLPEDCRDYAVVLKRYA 608
OY 301 DKYINISMKHPQEMKTYSLSPDSLFSAVKNFTETLASKSERLODFDKSNPILLRMNQOL 360
DB 609 DKYISISMKHPQEMKTYSVSPDSLFSAVKNFTETLASKSERLODFDKSNPILLRMNQOL 668
OY 361 MFLERAFIDPLGLPRPPYRHYIYAPSSHNKYAGSPFGITDALFDIESKYDPSKMGDV 420
DB 669 MFLERAFIDPLGLPRPPYRHYIYAPSSHNKYAGSPFGITDALFDIESKYDPSKMGDV 728
OY 421 KROIISAAFTVOAAETLSEVA 442
DB 729 KROIISAAFTVOAAETLSEVA 750

RESULT 6
US-09-895-793-944
Sequence 944, Application US/09895793
Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 944
LENGTH: 750
TYPE: PRT
ORGANISM: Homo sapiens
US-09-895-793-944

Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPDSSWRGSLKSYNVGPGFTGNFSTQKVMHISTNEVRIYVIGTLGAVEP 60
Db 309 MGSAPDSSWRGSLKSYNVGPGFTGNFSTQKVMHISTNEVRIYVIGTLGAVEP 368
QY 61 DRYVILGHRBQSWFVGGLDPOSGAAVHEIVASFEITLKEGRRPRITLFSWDAEEFGL 120
Db 369 DRYVILGHRBQSWFVGGLDPOSGAAVHEIVASFEITLKEGRRPRITLFSWDAEEFGL 428
QY 121 LGSTWADNRSRLLOERGVAVIYNDSIEGNVTLVDCTPLMTSYVYNLTLEKSPDGEF 180
Db 429 LGSTWADNRSRLLOERGVAVIYNDSIEGNVTLVDCTPLMTSYVYNLTLEKSPDGEF 488
QY 181 EGKSLYESWTKSPSPESGMPRIKSLGSGNDFEVFORLGIASGRARYTKMETNKEFSG 240
Db 489 EGKSLYESWTKSPSPESGMPRIKSLGSGNDFEVFORLGIASGRARYTKMETNKEFSG 548
QY 241 YPLHVSYTELEVKFIDPMPKHYLTVAOYRGGVFELANSIYLPFCRCRDYAVVLRKYA 300
Db 549 YPLHVSYTELEVKFIDPMPKHYLTVAOYRGGVFELANSIYLPFCRCRDYAVVLRKYA 608
QY 301 DKYINISKHPOEMKTYSLSPDSLSAVKNFTEIASKFSERLQDPDKSNPILRMANDOL 360
Db 609 DKYINISKHPOEMKTYSLSPDSLSAVKNFTEIASKFSERLQDPDKSNPILRMANDOL 668
QY 361 MFLERAFIDPLGLDPRPFYRHVIYAPSSHNKYAGSEFPIYDALFDEISKYDPSKMGDV 420
Db 669 MFLERAFIDPLGLDPRPFYRHVIYAPSSHNKYAGSEFPIYDALFDEISKYDPSKMGDV 728
QY 421 KRQISVAFTYQAAAETISEVA 442
Db 729 KRQISVAFTYQAAAETISEVA 750

RESULT 7

US-09-978-189-618
Sequence 618, Application US/09/978189
Publication No. US20030004102a1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978, 189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
 Best Local Similarity 98.0%; Pred. No. 7.3e-217;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

1 MGSAPPDSSWRGSLKVSYNVGPFTGNFSTQKVMHISTNEVTRIVNIGTLGAVEP 60
 |||||
 309 MGSAPPDSSWRGSLKVSYNVGPFTGNFSTQKVMHISTNEVTRIVNIGTLGAVEP 368
 |||||
 61 DRYVILGGRDMSWFGGIDPOSGAAVHEVRSFCTLKKEGRRPRTILFASMDAEFGL 120
 |||||
 369 DRYVILGGRDMSWFGGIDPOSGAAVHEVRSFCTLKKEGRRPRTILFASMDAEFGL 428
 |||||
 121 LGSTEWADNSRFLQERGVAYINADSSIEGNTLAVDCTPLMYSLVNULTEKSPDGEF 180
 |||||
 429 LGSTEWADNSRFLQERGVAYINADSSIEGNTLAVDCTPLMYSLVNULTEKSPDGEF 488
 |||||
 181 EKSLSYESWTKKSPSPERSGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMNETKFSG 240
 |||||
 489 EKSLSYESWTKKSPSPERSGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMNETKFSG 548
 |||||
 241 YPLYSVYETTELVEKFDPMFKYHLVVAQVRGAVFELANSIVLPDCRDYAVYLKRYA 300
 |||||
 549 YPLYSVYETTELVEKFDPMFKYHLVVAQVRGAVFELANSIVLPDCRDYAVYLKRYA 608
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 301 DKYINYSMKHPQDMKTYSLSPDSLSAVNFTETIASKESERLODPDKSPYILRMNDOL 360
 |||||
 609 DKYINYSMKHPQDMKTYSLSPDSLSAVNFTETIASKESERLODPDKSPYILRMNDOL 668
 |||||
 361 MFLERAFIDPLGPDPRFYRHVYIAPSSHNKYAGESFPDIYDALDESKVDPKAMGDV 420
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 669 MFLERAFIDPLGPDPRFYRHVYIAPSSHNKYAGESFPDIYDALDESKVDPKAMGDV 728
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 421 KROISVAFTVOAAETLSEVA 442
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 729 KROISVAFTVOAAETLSEVA 750
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RESULT 8
 US-09-978-608A-618
 ; Sequence 618, Application US/09978608A
 ; Publication No. US20030045462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Flivaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey J.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

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/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James.
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC22
/ CURRENT APPLICATION NUMBER: US/09/978, 608A
/ NUMBER OF SEQ ID NOS: 624
/ PRIOR Application removed - See File Wrapper or Palm
/ SEQ ID NO 618
/ LENGTH: 750
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-978-608A-618
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Query Match          98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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1 MGSAAPPSSWMSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 MGSAAPPSSWMSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 368
61 DRYVILGHRDSWVGGIDPOSGAAVHEIYVSFGTLKEGRRPRTILFASWDAEEFGL 120
DRYVILGHRDSWVGGIDPOSGAAVHEIYVSFGTLKEGRRPRTILFASWDAEEFGL 428
121 LGSTMAEDNSRLQERGVAYINADSIENNTLRVDCPTPLVYSLVYNTLTKELKSPDEGF 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 LGSTMAEDNSRLQERGVAYINADSIENNTLRVDCPTPLVYSLVYNTLTKELKSPDEGF 488
181 EGKSLYESWTKKSPSPESGMPRISKLSGNDFEVFFQRLGIASGRARTKMWETNKESG 240
EGKSLYESWTKKSPSPESGMPRISKLSGNDFEVFFQRLGIASGRARTKMWETNKESG 548
241 YPLHSVYETIELVEKFTDPMFKYHLTVAAOVGAGWVFEIANSIVLPDRCRDYAVVLRKYA 300
YPLHSVYETIELVEKFTDPMFKYHLTVAAOVGAGWVFEIANSIVLPDRCRDYAVVLRKYA 608
301 DKIVNISMKHPQEMKTYSLSPDLSFSAVKNFTEIASKFSERLQDDPKSNPILRRMNDQL 360
DKIVNISMKHPQEMKTYSLSPDLSFSAVKNFTEIASKFSERLQDDPKSNPILRRMNDQL 668
609 DKIVNISMKHPQEMKTYSLSPDLSFSAVKNFTEIASKFSERLQDDPKSNPILRRMNDQL 668
361 MFLERAFIDPLGLPRPFYRHVITYAPSSHNKYGESFPGIYDALDIESKVPDSKAWGDY 420
MFLERAFIDPLGLPRPFYRHVITYAPSSHNKYGESFPGIYDALDIESKVPDSKAWGDY 728
669 MFLERAFIDPLGLPRPFYRHVITYAPSSHNKYGESFPGIYDALDIESKVPDSKAWGDY 728
421 KROIYVAAFTVOAAAEITLSEVA 442
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729 KROIYVAAFTVOAAAEITLSEVA 750
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RESULT 9
US-09-978-585A-618
/ Sequence 618, Application US/09/978585A
/ Publication No. US20030049633A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
```

```
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerlitsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavini, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James.
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630PIC15
/ CURRENT APPLICATION NUMBER: US/09/978, 585A
/ NUMBER OF SEQ ID NOS: 624
/ PRIOR Application removed - See File Wrapper or Palm
/ SEQ ID NO 618
/ LENGTH: 750
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-978-585A-618
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Query Match          98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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1 MGSAAPPSSWMSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 60
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309 MGSAAPPSSWMSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 368
61 DRYVILGHRDSWVGGIDPOSGAAVHEIYVSFGTLKEGRRPRTILFASWDAEEFGL 120
DRYVILGHRDSWVGGIDPOSGAAVHEIYVSFGTLKEGRRPRTILFASWDAEEFGL 428
121 LGSTMAEDNSRLQERGVAYINADSIENNTLRVDCPTPLVYSLVYNTLTKELKSPDEGF 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 LGSTMAEDNSRLQERGVAYINADSIENNTLRVDCPTPLVYSLVYNTLTKELKSPDEGF 488
181 EGKSLYESWTKKSPSPESGMPRISKLSGNDFEVFFQRLGIASGRARTKMWETNKESG 240
EGKSLYESWTKKSPSPESGMPRISKLSGNDFEVFFQRLGIASGRARTKMWETNKESG 548
241 YPLHSVYETIELVEKFTDPMFKYHLTVAAOVGAGWVFEIANSIVLPDRCRDYAVVLRKYA 300
YPLHSVYETIELVEKFTDPMFKYHLTVAAOVGAGWVFEIANSIVLPDRCRDYAVVLRKYA 608
301 DKIVNISMKHPQEMKTYSLSPDLSFSAVKNFTEIASKFSERLQDDPKSNPILRRMNDQL 360
DKIVNISMKHPQEMKTYSLSPDLSFSAVKNFTEIASKFSERLQDDPKSNPILRRMNDQL 668
609 DKIVNISMKHPQEMKTYSLSPDLSFSAVKNFTEIASKFSERLQDDPKSNPILRRMNDQL 668
361 MFLERAFIDPLGLPRPFYRHVITYAPSSHNKYGESFPGIYDALDIESKVPDSKAWGDY 420
MFLERAFIDPLGLPRPFYRHVITYAPSSHNKYGESFPGIYDALDIESKVPDSKAWGDY 728
669 MFLERAFIDPLGLPRPFYRHVITYAPSSHNKYGESFPGIYDALDIESKVPDSKAWGDY 728
421 KROIYVAAFTVOAAAEITLSEVA 442
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
729 KROIYVAAFTVOAAAEITLSEVA 750
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RESULT 10

US-09-978-191A-618
 : Sequence 618. Application US/09978191A
 : Publication No. US20030050239A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Deanoysers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gertisen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kijavlin, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James;
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2630P1C4
 : CURRENT APPLICATION NUMBER: US/09/978.191A
 : PRIOR FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 09/918585
 : PRIOR FILING DATE: 2001-07-30
 : PRIOR APPLICATION NUMBER: 60/062250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/064249
 : PRIOR FILING DATE: 1997-11-03
 : PRIOR APPLICATION NUMBER: 60/065311
 : PRIOR FILING DATE: 1997-11-13
 : PRIOR APPLICATION NUMBER: 60/066364
 : PRIOR FILING DATE: 1997-11-21
 : PRIOR APPLICATION NUMBER: 60/077450
 : PRIOR FILING DATE: 1998-03-10
 : PRIOR APPLICATION NUMBER: 60/077632
 : PRIOR FILING DATE: 1998-03-11
 : PRIOR APPLICATION NUMBER: 60/077641
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 : PRIOR APPLICATION NUMBER: 60/077649
 : PRIOR FILING DATE: 1998-03-11
 : PRIOR APPLICATION NUMBER: 60/077791
 : PRIOR FILING DATE: 1998-03-12
 : PRIOR APPLICATION NUMBER: 60/078004
 : PRIOR FILING DATE: 1998-03-13
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 : PRIOR FILING DATE: 1998-03-20
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 : PRIOR FILING DATE: 1998-03-20
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 : PRIOR FILING DATE: 1998-03-20
 : PRIOR APPLICATION NUMBER: 60/079294
 : PRIOR FILING DATE: 1998-03-25
 : PRIOR APPLICATION NUMBER: 60/079656
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 : PRIOR APPLICATION NUMBER: 60/079664
 : PRIOR FILING DATE: 1998-03-27
 : PRIOR APPLICATION NUMBER: 60/079689

: PRIOR FILING DATE: 1998-03-27
 : PRIOR APPLICATION NUMBER: 60/079663
 : PRIOR FILING DATE: 1998-03-27
 : PRIOR APPLICATION NUMBER: 60/079728
 : PRIOR FILING DATE: 1998-03-27
 : PRIOR APPLICATION NUMBER: 60/079786
 : PRIOR FILING DATE: 1998-03-27
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 : PRIOR FILING DATE: 1998-03-30
 : PRIOR APPLICATION NUMBER: 60/079923
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 : PRIOR FILING DATE: 1998-03-31
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 : PRIOR FILING DATE: 1998-04-08
 : PRIOR APPLICATION NUMBER: 60/081195
 : PRIOR FILING DATE: 1998-04-08
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 : PRIOR FILING DATE: 1998-04-09
 : PRIOR APPLICATION NUMBER: 60/081229
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 : PRIOR FILING DATE: 1998-04-15
 : PRIOR APPLICATION NUMBER: 60/081817
 : PRIOR FILING DATE: 1998-04-15
 : PRIOR APPLICATION NUMBER: 60/081819
 : PRIOR FILING DATE: 1998-04-15
 : PRIOR APPLICATION NUMBER: 60/081952
 : PRIOR FILING DATE: 1998-04-15
 : PRIOR APPLICATION NUMBER: 60/081838
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 : PRIOR APPLICATION NUMBER: 60/082568
 : PRIOR FILING DATE: 1998-04-21
 : PRIOR APPLICATION NUMBER: 60/082569
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 : PRIOR APPLICATION NUMBER: 60/082704
 : PRIOR FILING DATE: 1998-04-22
 : PRIOR APPLICATION NUMBER: 60/082804
 : PRIOR FILING DATE: 1998-04-22
 : PRIOR APPLICATION NUMBER: 60/082700
 : PRIOR FILING DATE: 1998-04-22
 : PRIOR APPLICATION NUMBER: 60/082797
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 : PRIOR APPLICATION NUMBER: 60/083336
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 : PRIOR FILING DATE: 1998-04-28
 : PRIOR APPLICATION NUMBER: 60/083392
 : PRIOR FILING DATE: 1998-04-29
 : PRIOR APPLICATION NUMBER: 60/083495
 : PRIOR FILING DATE: 1998-04-29
 : PRIOR APPLICATION NUMBER: 60/083496
 : PRIOR FILING DATE: 1998-04-29

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PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match          98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7, 3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPRPPSSMKGSLKVSINVGPGFTGNFSTOKVKMHINHSNEDVRIYVIGTLRGAVDP 60
    |||||||
DB 309 MGSAPRPPSSMKGSLKVSINVGPGFTGNFSTOKVKMHINHSNEDVRIYVIGTLRGAVDP 368
    |||||||
QY 61 DRYVILGHRDQSVNGGIDPQSGAAYVHEHTVBSFGTLKKGMRPRTILFASMDAEEPL 120
    |||||||
DB 369 DRYVILGHRDQSVNGGIDPQSGAAYVHEHTVBSFGTLKKGMRPRTILFASMDAEEPL 428
    |||||||
QY 121 LGSTWAEADNSRLDERGVAYINADSSLEGNTLRVDTPLMYSLVYNLTKEIKSPDEGF 180
    |||||||
DB 429 LGSTWAEADNSRLDERGVAYINADSSLEGNTLRVDTPLMYSLVYNLTKEIKSPDEGF 488
    |||||||
QY 181 ECKSLYESWTKKSPSPERFSGMPRISKLGSGNDEVEFPQRLGIASGRARYTKMNETKFSG 240
    |||||||
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|||||
DB 489 ECKSLYESWTKKSPSPERFSGMPRISKLGSGNDEVEFPQRLGIASGRARYTKMNETKFSG 548
    |||||||
QY 241 YPLVHSVYETVELVEKFPYDPMFKYHLLTVNOVRGMPFELANSIVLPDCCDYAVVLKRYA 300
    |||||||
DB 549 YPLVHSVYETVELVEKFPYDPMFKYHLLTVNOVRGMPFELANSIVLPDCCDYAVVLKRYA 608
    |||||||
QY 301 DKTYINSMKHPOEMKTYSLSFDSLFSVKNFTETASKFSERLQDPDKSNPILLRMMNDOL 360
    |||||||
DB 609 DKTYISMKHPOEMKTYSLSFDSLFSVKNFTETASKFSERLQDPDKSNPILLRMMNDOL 668
    |||||||
QY 361 MFLERAFIDPLGUPDRPFYRHHVYIAPSSHNKYGESFPGIYDALFDIESKVDPSKAMGDV 420
    |||||||
DB 669 MFLERAFIDPLGUPDRPFYRHHVYIAPSSHNKYGESFPGIYDALFDIESKVDPSKAMGEV 728
    |||||||
QY 421 KROIYVAFTVQAAETLSFVA 442
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DB 729 KROIYVAFTVQAAETLSFVA 750
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RESULT 11
US-09-978-403A-618
Sequence 618, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077649	PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/077791	PRIOR FILING DATE: 1998-03-12	PRIOR APPLICATION NUMBER: 60/078004	PRIOR FILING DATE: 1998-03-13	PRIOR APPLICATION NUMBER: 60/078886	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078936	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078939	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-03-25	PRIOR APPLICATION NUMBER: 60/079656	PRIOR FILING DATE: 1998-03-26	PRIOR APPLICATION NUMBER: 60/079664	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079689	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079663	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079728	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079786	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079920	PRIOR FILING DATE: 1998-03-30	PRIOR APPLICATION NUMBER: 60/079923	PRIOR FILING DATE: 1998-03-30	PRIOR APPLICATION NUMBER: 60/080105	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080107	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080165	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080194	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080327	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080328	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080333	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080334	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/081070	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081071	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081195	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081203	PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081555	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082565
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1	PRIOR FILING DATE: 1998-04-21
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4	PRIOR APPLICATION NUMBER: 60/082804
5	PRIOR FILING DATE: 1998-04-22
6	PRIOR APPLICATION NUMBER: 60/082700
7	PRIOR FILING DATE: 1998-04-22
8	PRIOR APPLICATION NUMBER: 60/082797
9	PRIOR FILING DATE: 1998-04-22
10	PRIOR APPLICATION NUMBER: 60/082796
11	PRIOR FILING DATE: 1998-04-23
12	PRIOR APPLICATION NUMBER: 60/083336
13	PRIOR FILING DATE: 1998-04-27
14	PRIOR APPLICATION NUMBER: 60/083332
15	PRIOR FILING DATE: 1998-04-28
16	PRIOR APPLICATION NUMBER: 60/083392
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18	PRIOR APPLICATION NUMBER: 60/083495
19	PRIOR FILING DATE: 1998-04-29
20	PRIOR APPLICATION NUMBER: 60/083496
21	PRIOR FILING DATE: 1998-04-29
22	PRIOR APPLICATION NUMBER: 60/083499
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24	PRIOR APPLICATION NUMBER: 60/083545
25	PRIOR FILING DATE: 1998-04-29
26	PRIOR APPLICATION NUMBER: 60/083554
27	PRIOR FILING DATE: 1998-04-29
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32	PRIOR APPLICATION NUMBER: 60/083500
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35	PRIOR FILING DATE: 1998-04-30
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38	PRIOR APPLICATION NUMBER: 60/084414
39	PRIOR FILING DATE: 1998-05-06
40	PRIOR APPLICATION NUMBER: 60/084441
41	PRIOR FILING DATE: 1998-05-06
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43	PRIOR FILING DATE: 1998-05-07
44	PRIOR APPLICATION NUMBER: 60/084639
45	PRIOR FILING DATE: 1998-05-07
46	PRIOR APPLICATION NUMBER: 60/084640
47	PRIOR FILING DATE: 1998-05-07
48	PRIOR APPLICATION NUMBER: 60/084598
49	PRIOR FILING DATE: 1998-05-07
50	PRIOR APPLICATION NUMBER: 60/084600
51	PRIOR FILING DATE: 1998-05-07
52	PRIOR APPLICATION NUMBER: 60/084627
53	PRIOR FILING DATE: 1998-05-07
54	PRIOR APPLICATION NUMBER: 60/084643
55	PRIOR FILING DATE: 1998-05-07
56	PRIOR APPLICATION NUMBER: 60/085339
57	PRIOR FILING DATE: 1998-05-13
58	PRIOR APPLICATION NUMBER: 60/085338
59	PRIOR FILING DATE: 1998-05-13
60	PRIOR APPLICATION NUMBER: 60/085323
61	PRIOR FILING DATE: 1998-05-13
62	PRIOR APPLICATION NUMBER: 60/085582
63	PRIOR FILING DATE: 1998-05-15
64	PRIOR APPLICATION NUMBER: 60/085700
65	PRIOR FILING DATE: 1998-05-15
66	PRIOR APPLICATION NUMBER: 60/085699
67	PRIOR FILING DATE: 1998-05-15
68	PRIOR APPLICATION NUMBER: 60/085797
69	PRIOR FILING DATE: 1998-05-15
70	PRIOR APPLICATION NUMBER: 60/085580
71	PRIOR FILING DATE: 1998-05-15
72	PRIOR APPLICATION NUMBER: 60/085573
73	PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
 Best Local Similarity 98.0%; Pred. No. 7.3e-217;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAAPPSSWNGSLKVSYNVGPFGTGNFSTQKVMHHTSTEVRIYINVTGLGAVEP 60
 DB 309 MGSAAPPSSWNGSLKVPYNGPFTGNFSTQKVMHHTSTEVRIYINVTGLGAVEP 368
 QY 61 DRYVILGHRDSWVEGIDPOGSAVHETVASFCTLKEGMRPRTTLFASWDAEEFGL 120
 DB 369 DRYVILGHRDSWVEGIDPOGSAVHETVASFCTLKEGMRPRTTLFASWDAEEFGL 428
 QY 121 LGSTMAEDNSLLOERGVAYINADSSIEGNTLVDCPTPLMYSLVNLTKEKSPDEGF 180
 DB 429 LGSTMAEDNSLLOERGVAYINADSSIEGNTLVDCPTPLMYSLVNLTKEKSPDEGF 488
 QY 181 BGKSLYEEMTKKSPSPFSGMFRISKLGSNDFFVFORLGIASGRARTKMTNKFSG 240
 DB 489 BGKSLYEEMTKKSPSPFSGMFRISKLGSNDFFVFORLGIASGRARTKMTNKFSG 548
 QY 241 YPLXSVYETVELYEKFDYDPMKXHLTVAYVGGVAFELANSIVLPDCRDYAVVLRKYA 300
 DB 549 YPLXSVYETVELYEKFDYDPMKXHLTVAYVGGVAFELANSIVLPDCRDYAVVLRKYA 608
 QY 301 DKIVYSKHHQEMKTYISLSPDSLFSAVKNFTLKSERLQDPDKSNPILRRMNDOL 360
 DB 609 DKIVYSKHHQEMKTYISLSPDSLFSAVKNFTLKSERLQDPDKSNPILRRMNDOL 668
 QY 361 MFLKFAFDPLGLPRPRYRHITYAPSSHNKXAGSPGIYALDIDSKVPSKAMGVY 420
 DB 669 MFLKFAFDPLGLPRPRYRHITYAPSSHNKXAGSPGIYALDIDSKVPSKAMGVY 728
 QY 421 KRQISVAAFYVQAAETLSEVA 442
 DB 729 KRQISVAAFYVQAAETLSEVA 750

RESULT 12
 US-09-978-564A-618
 Sequence 618, Application US/09978564A
 Publication No. US20030050241A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
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 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavita, Ivar J.
 APPLICANT: Kuo, Sophia S.
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 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC25
 CURRENT FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSWRGSLKSYNVGPGFTGNFSTQKMKHHSNEVTRYNYIGTLRGAVEP 60
DB 309 MGSAPPDSSWRGSLKPYNVGPGFTGNFSTQKMKHHSNEVTRYNYIGTLRGAVEP 368
QY 61 DRYVILGHRDSWYFGGIDPOSGAAVYHEVYRSFGTLKKEGMRPRRTILFASMPAEFGL 120
DB 369 DRYVILGHRDSWYFGGIDPOSGAAVYHEVYRSFGTLKKEGMRPRRTILFASMPAEFGL 428
QY 121 LGSTWMAEDNSRLQERGVAYINADSSIEGNYTLRVDCPTPLMSLVYNLTKELKSPDEGF 180
DB 429 LGSTWMAEDNSRLQERGVAYINADSSIEGNYTLRVDCPTPLMSLVYNLTKELKSPDEGF 488
QY 181 EGKSLYSWTKKSSPFSGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMNTNFKFSG 240
DB 489 EGKSLYSWTKKSSPFSGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMNTNFKFSG 548
QY 241 YPLXHSYETEYELVEKYDDPMFKYHLTVAGYRGSMVELANSIYLPDPCRDYAVYLKRYA 300
DB 549 YPLXHSYETEYELVEKYDDPMFKYHLTVAGYRGSMVELANSIYLPDPCRDYAVYLKRYA 608
QY 301 DKIVNISMKHQEMKTYSLSEFSLFSAVNKFTETASKFSERLQDFDKSNPILLRMNDOL 360
DB 609 DKIVNISMKHQEMKTYSVSPDSLFSAVKNFTETASKFSERLQDFDKSNPILLRMNDOL 668
QY 361 MFLERATIDPLGLDPRFRYRVIYIAPSSHNKYAGESPGLYDALFDIESKYVDPKANGDV 420
DB 669 MFLERATIDPLGLDPRFRYRVIYIAPSSHNKYAGESPGLYDALFDIESKYVDPKANGDV 728
QY 421 KROISVAAFYVOAAETLSEYA 442
DB 729 KROLYVAATFYVOAAETLSEYA 750

RESULT 13
US-09-999-833A-618
Sequence 618, Application US/09999833A
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnayers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Olang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2% Score 2288; DB 11; Length 750;
Best Local Similarity 98.0% Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

1 MGSAPPDSSWMSGLKVSYNVNGPGFTGNFSTOKVKMHIHSTNEVTRIYNVIGTLGAVEP 60
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61 DRYVLGGHRSWVGGLDPOSGAAVVEHYRSFETLKEGRRPRTILFASWDAEEGL 120
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369 DRYVLGGHRSWVGGLDPOSGAAVVEHYRSFETLKEGRRPRTILFASWDAEEGL 428
121 LGSTFMAEDNSRLQERGVAYINADSSIEGNVTLVDCSTPLMYSIVYNUITELKSPDGEF 180
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429 LGSTFMAEDNSRLQERGVAYINADSSIEGNVTLVDCSTPLMYSIVYNUITELKSPDGEF 488
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|||||
489 EGKSLYESWTKKSPSPERSGMPRIKSLGSGNDEFEVFPORLGIASGRARYTNMETNKGSG 548
241 YPLHYSVETELVEKFTDPMFKYHLYAQRGAGVFEELANSIVLPCCRDYAVVLKRYA 300
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549 YPLHYSVETELVEKFTDPMFKYHLYAQRGAGVFEELANSIVLPCCRDYAVVLKRYA 608
301 DKYIVISKHPQEMKTYISLFSDSLFSAYKNFTETLASKSESRLODPDKSNPILRMNOL 360
|||||
609 DKYIVISKHPQEMKTYISLFSDSLFSAYKNFTETLASKSESRLODPDKSNPILRMNOL 668

361 MFLERAFIDPLGLPDRPPYRHVYVAPSSHNKYAGSEFPGIYDALFDIESKYDPSKMGDV 420
|||||
669 MFLERAFIDPLGLPDRPPYRHVYVAPSSHNKYAGSEFPGIYDALFDIESKYDPSKMGDV 728
421 KRQISVAAPFYVQAAAEITLSEVA 442
|||||
729 KRQIVAAFTVQAAAEITLSEVA 750
RESULT 14
US-09-981-915A-618
; Sequence 618, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
 Best Local Similarity 98.0%; Pred. No. 7 3e-217;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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 Db 369 DRYVILGHRDSWVFGIDPQSGAAVYHETVRSFGLTKEGMRPRRTILFASMDAEFGL 428
 QY 121 LGSTFMAEDNSRLLOERGVAYINADSSIEGNYTLRVDCPTLMYSLYNLTLEKSPDEGF 180
 Db 429 LGSTFMAEDNSRLLOERGVAYINADSSIEGNYTLRVDCPTLMYSLYNLTLEKSPDEGF 488
 QY 181 EGKSLYESWTKKSPSPESGMRPRISKLGSNDPFEYFORLFIASGRARYTNMWNENKESG 240
 Db 489 EGKSLYESWTKKSPSPESGMRPRISKLGSNDPFEYFORLFIASGRARYTNMWNENKESG 548
 QY 241 YPLVHSYVETELVEKFEYDPMFKYHLTVAAQVGGKWFELANSIVLPDCRDYAVVLRKYA 300
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 QY 301 DKITNISKHHQEKTYLSLFSDFSAVKNFTETLASKTSEERLODFDKSNPTILRRMNDOL 360
 Db 609 DKITNISKHHQEKTYLSLFSDFSAVKNFTETLASKTSEERLODFDKSNPTILRRMNDOL 668
 QY 361 MELEAFIDPLGLPDRPYRHVYAPSSHNKYAGSPFGIYDALFDIESKYDPSKMGDV 420
 Db 669 MELEAFIDPLGLPDRPYRHVYAPSSHNKYAGSPFGIYDALFDIESKYDPSKMGDV 728
 QY 421 KROIISVAFTVQAAAEITLSEVA 442
 Db 729 KROIISVAFTVQAAAEITLSEVA 750
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 ; Sequence 618, Application US/09978824
 ; Publication No. US20030055216a1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Bolstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paonl, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C14
 CURRENT APPLICATION NUMBER: US/09/978,824
 CURRENT FILING DATE: 2001-10-17
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Query Match 98.28; Score 2288; DB 11; Length 750;
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 QY 181 EGKSLYSWTKSPSPFSGMPRTSKLGSNDPEVFQORGLASGRARYTKNETNFSG 240
 DB 489 EGKSLYSWTKSPSPFSGMPRTSKLGSNDPEVFQORGLASGRARYTKNETNFSG 548
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 DB 609 DKTYNISMKHPQEMKITYLSFSDSLFSAVKNFTELAKFSERLQDFDKSNPILRMANDOL 668
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 DB 669 MFLERAFIDPLGDRPFYRHVITYAPSSHNKYAGESPGIYDALFDESRYVDSKANGDV 728
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 DB 729 KRQISVAFTVQAAAEFLSEVA 750

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 Job time : 60 secs

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GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: October 4, 2003, 23:20:12 ; Search time 35 Seconds
(without alignments)
534.326 Million cell updates/sec

Title: US-09-973-382C-2

Perfect score: 2329
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Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	2288	98.2	707	1	US-08-528-122-18		Sequence 18, Appl
	2	2288	98.2	707	5	PCT-US95-11720-18		Sequence 18, Appl
	3	2288	98.2	750	1	US-08-325-553-2		Sequence 2, Appl
	4	2288	98.2	750	2	US-08-394-152A-2		Sequence 2, Appl
	5	2288	98.2	750	3	US-09-044-668-2		Sequence 2, Appl
	6	2288	98.2	750	4	US-08-705-477E-2		Sequence 2, Appl
	7	2281	97.9	693	4	US-08-705-477E-101		Sequence 101, App
	8	445.5	19.1	622	1	US-08-547-197-1		Sequence 1, Appl
	9	445.5	19.1	622	3	US-08-957-940-1		Sequence 1, Appl
	10	425	18.2	760	3	US-08-547-197-2		Sequence 2, Appl
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	13	131.5	5.6	481	3	US-09-330-095-1		Sequence 1, Appl
	14	122.5	5.3	473	4	US-09-482-273-120		Sequence 120, App
	15	121.5	5.2	584	4	US-09-252-991A-18292		Sequence 18292, A
	16	119	5.1	718	4	US-09-252-991A-27540		Sequence 27540, A
	17	111	4.8	537	4	US-09-079-955-5		Sequence 5, Appl
	18	107.5	4.6	1447	4	US-09-376-330-17		Sequence 17, Appl
	19	103	4.4	873	4	US-09-252-991A-30504		Sequence 30504, A
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	21	100.5	4.3	613	4	US-09-712-266-5		Sequence 5, Appl
	22	100.5	4.3	613	4	US-09-091-889A-2		Sequence 2, Appl
	23	100	4.3	19	1	US-08-325-553-11		Sequence 11, Appl
	24	100	4.3	19	2	US-08-394-152A-11		Sequence 11, Appl
	25	100	4.3	19	4	US-08-705-477E-11		Sequence 11, Appl
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33	96	4.1	396	4	US-09-575-205-2	Sequence 2, Appl
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41	93.5	4.0	2233	3	US-08-569-853-2	Sequence 2, Appl
42	93.5	4.0	2233	3	US-08-987-439-1	Sequence 1, Appl
43	91.5	3.9	1151	4	US-09-134-001C-3242	Sequence 3242, Ap
44	91	3.9	514	2	US-08-865-311-2	Sequence 2, Appl
45	91	3.9	514	4	US-09-315-720-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-528-122-18
Sequence 18, Application US/08528122
Patent No. 5726044
GENERAL INFORMATION:
APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,122
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..707
OTHER INFORMATION: /note= "EXTRACELLULAR DOMAIN OF
OTHER INFORMATION: PSMA"
US-08-528-122-18
Query Match 98.2%; Score 2288; DB 1; Length 707;

APPLICATION NUMBER: US/07/973.337A
FILING DATE: 05 NOV 1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/41426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-325-553-2

Query Match 98.2%; Score 2288; DB 1; Length 750;
Best Local Similarity 98.0%; Pred. No. 1.8e-214;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSWRGSLKAVYVNGPFGTGNSTOKYKMHISTNEYTRYNYIGTLKGAVER 60
DB 309 MGSAPPDSSWRGSLKAVYVNGPFGTGNSTOKYKMHISTNEYTRYNYIGTLKGAVER 368
QY 61 DRVYILGCHDMSWFGGIDPOSGAAYVHEIVRSFGTLKKGWPRRTILFASMDAEFGL 120
DB 369 DRVYILGCHDMSWFGGIDPOSGAAYVHEIVRSFGTLKKGWPRRTILFASMDAEFGL 428
QY 121 LGSTEWAEADNSRLLOEGRVAVINADSSIEGNYTLRVDCPTPLMTSLVYNTLRELKSPDEGF 180
DB 429 LGSTEWAEADNSRLLOEGRVAVINADSSIEGNYTLRVDCPTPLMTSLVYNTLRELKSPDEGF 488
QY 181 EGSLSYSWTKKSPSPFSGMPRIKSLGSGNDEVEFQRIASGRARYTKNMTNFGS 240
DB 489 EGSLSYSWTKKSPSPFSGMPRIKSLGSGNDEVEFQRIASGRARYTKNMTNFGS 548
QY 241 YPLHSYETVELVEKEDYDPMFKYHLTVAVOGRGMVELANSIYLPDCRDYAVVLKRYA 300
DB 549 YPLHSYETVELVEKEDYDPMFKYHLTVAVOGRGMVELANSIYLPDCRDYAVVLKRYA 608
QY 301 DKTYINSMKHPQEMKTYSLSPDSLFSVKNFTETIASKFSERLQDFKSNPILLRMNDQL 360
DB 609 DKTYINSMKHPQEMKTYSLSPDSLFSVKNFTETIASKFSERLQDFKSNPILLRMNDQL 668
QY 361 MFLERAFIDPLGIDPRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDV 420
DB 669 MFLERAFIDPLGIDPRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDV 728
QY 421 KROIYVAFTVOAAAEITLSEVA 442
DB 729 KROIYVAFTVOAAAEITLSEVA 750

RESULT 4
US-08-394-152A-2
Sequence 2, Application US/08394152A
Patent No. 5935818

GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heslon, Warren D.W.
APPLICANT: Falt, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 750 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-394-152A-2

Query Match 98.2%; Score 2288; DB 2; Length 750;
Best Local Similarity 98.0%; Pred. No. 1.8e-214;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSWRGSLKAVYVNGPFGTGNSTOKYKMHISTNEYTRYNYIGTLKGAVER 60
DB 309 MGSAPPDSSWRGSLKAVYVNGPFGTGNSTOKYKMHISTNEYTRYNYIGTLKGAVER 368
QY 61 DRVYILGCHDMSWFGGIDPOSGAAYVHEIVRSFGTLKKGWPRRTILFASMDAEFGL 120
DB 369 DRVYILGCHDMSWFGGIDPOSGAAYVHEIVRSFGTLKKGWPRRTILFASMDAEFGL 428
QY 121 LGSTEWAEADNSRLLOEGRVAVINADSSIEGNYTLRVDCPTPLMTSLVYNTLRELKSPDEGF 180
DB 429 LGSTEWAEADNSRLLOEGRVAVINADSSIEGNYTLRVDCPTPLMTSLVYNTLRELKSPDEGF 488
QY 181 EGSLSYSWTKKSPSPFSGMPRIKSLGSGNDEVEFQRIASGRARYTKNMTNFGS 240
DB 489 EGSLSYSWTKKSPSPFSGMPRIKSLGSGNDEVEFQRIASGRARYTKNMTNFGS 548
QY 241 YPLHSYETVELVEKEDYDPMFKYHLTVAVOGRGMVELANSIYLPDCRDYAVVLKRYA 300
DB 549 YPLHSYETVELVEKEDYDPMFKYHLTVAVOGRGMVELANSIYLPDCRDYAVVLKRYA 608
QY 301 DKTYINSMKHPQEMKTYSLSPDSLFSVKNFTETIASKFSERLQDFKSNPILLRMNDQL 360
DB 609 DKTYINSMKHPQEMKTYSLSPDSLFSVKNFTETIASKFSERLQDFKSNPILLRMNDQL 668
QY 361 MFLERAFIDPLGIDPRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDV 420
DB 669 MFLERAFIDPLGIDPRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDV 728
QY 421 KROIYVAFTVOAAAEITLSEVA 442
DB 729 KROIYVAFTVOAAAEITLSEVA 750

RESULT 5
US-09-044-668-2
Sequence 2, Application US/09044668
Patent No. 6150508

GENERAL INFORMATION:
APPLICANT: Murphy, Gerald P.
APPLICANT: Boynton, Alton L.
APPLICANT: Holmes, Eric H.
APPLICANT: Tino, William Thomas
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: FOR THE EXTRACELLULAR DOMAIN OF PROSTATE-SPECIFIC
MEMBRANE ANTIGEN

; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds, LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/044,668
 ; FILING DATE: 18-MAR-1998
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baldwin, Geraldine F
 ; REGISTRATION NUMBER: 31,232
 ; REFERENCE/DOCKET NUMBER: 8511-0013-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 750 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6150508e
 ; US-09-044-668-2

Query Match 98.2%; Score 2288; DB 3; Length 750;
 Best Local Similarity 98.0%; Pred. No. 1,8e-214;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPDPSWRSGLKVSYPGFTGNFSTOKVGMHISTNEVRIYVIGTLGAVEP 60
 DB 309 MGSAPDPSWRSGLKVSYPGFTGNFSTOKVGMHISTNEVRIYVIGTLGAVEP 368
 QY 61 DRYVILGGRDSWVEGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEEFGL 120
 DB 369 DRYVILGGRDSWVEGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEEFGL 428
 QY 121 LGSTWADNSRLLOERGVAYINADSSIEGNTTLVDCDTPLMYSLVYHNLTKELKSPDEGF 180
 DB 429 LGSTWADNSRLLOERGVAYINADSSIEGNTTLVDCDTPLMYSLVYHNLTKELKSPDEGF 488
 QY 181 EKSLSYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTKMWTNKFSG 240
 DB 489 EKSLSYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTKMWTNKFSG 548
 QY 241 YPLYSVYETVELVEKFTDPMKHYLTVAYVGRGVFELANSIVLPFCRDYAAVLRKYA 300
 DB 549 YPLYSVYETVELVEKFTDPMKHYLTVAYVGRGVFELANSIVLPFCRDYAAVLRKYA 608
 QY 301 DKIVYISMKHPQEMKTYISFDSLSAYAKNFTELASKSESRLODPDKSNPIYLRRMNDOL 360
 DB 609 DKIVYISMKHPQEMKTYISFDSLSAYAKNFTELASKSESRLODPDKSNPIYLRRMNDOL 668
 QY 361 MFLERAFIDPLGLPRPRPYRHVYAPSSHNKYAGSFPGIYDALFDESKVDPKAMGDV 420
 DB 669 MFLERAFIDPLGLPRPRPYRHVYAPSSHNKYAGSFPGIYDALFDESKVDPKAMGDV 728
 QY 421 KROIYVAAFYVOAAETLSEVA 442
 DB 729 KROIYVAAFYVOAAETLSEVA 750

RESULT 6
 US-08-705-477E-2
 ; Sequence 2, Application US/08705477E
 ; Patent No. 6569432
 ; GENERAL INFORMATION:
 ; APPLICANT: Isreali, Ron S
 ; APPLICANT: Heston, Warren D.W.
 ; APPLICANT: Fair, William R.
 ; APPLICANT: Overfelli, Quathek
 ; APPLICANT: Pinto, John
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 1769/41426-G
 ; CURRENT APPLICATION NUMBER: US/08/705,477E
 ; CURRENT FILING DATE: 1996-08-29
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 750
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-705-477E-2

Query Match 98.2%; Score 2288; DB 4; Length 750;
 Best Local Similarity 98.0%; Pred. No. 1,8e-214;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPDPSWRSGLKVSYPGFTGNFSTOKVGMHISTNEVRIYVIGTLGAVEP 60
 DB 309 MGSAPDPSWRSGLKVSYPGFTGNFSTOKVGMHISTNEVRIYVIGTLGAVEP 368
 QY 61 DRYVILGGRDSWVEGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEEFGL 120
 DB 369 DRYVILGGRDSWVEGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEEFGL 428
 QY 121 LGSTWADNSRLLOERGVAYINADSSIEGNTTLVDCDTPLMYSLVYHNLTKELKSPDEGF 180
 DB 429 LGSTWADNSRLLOERGVAYINADSSIEGNTTLVDCDTPLMYSLVYHNLTKELKSPDEGF 488
 QY 181 EKSLSYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTKMWTNKFSG 240
 DB 489 EKSLSYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTKMWTNKFSG 548
 QY 241 YPLYSVYETVELVEKFTDPMKHYLTVAYVGRGVFELANSIVLPFCRDYAAVLRKYA 300
 DB 549 YPLYSVYETVELVEKFTDPMKHYLTVAYVGRGVFELANSIVLPFCRDYAAVLRKYA 608
 QY 301 DKIVYISMKHPQEMKTYISFDSLSAYAKNFTELASKSESRLODPDKSNPIYLRRMNDOL 360
 DB 609 DKIVYISMKHPQEMKTYISFDSLSAYAKNFTELASKSESRLODPDKSNPIYLRRMNDOL 668
 QY 361 MFLERAFIDPLGLPRPRPYRHVYAPSSHNKYAGSFPGIYDALFDESKVDPKAMGDV 420
 DB 669 MFLERAFIDPLGLPRPRPYRHVYAPSSHNKYAGSFPGIYDALFDESKVDPKAMGDV 728
 QY 421 KROIYVAAFYVOAAETLSEVA 442
 DB 729 KROIYVAAFYVOAAETLSEVA 750

RESULT 7
 US-08-705-477E-101
 ; Sequence 101, Application US/08705477E
 ; Patent No. 6569432
 ; GENERAL INFORMATION:
 ; APPLICANT: Isreali, Ron S
 ; APPLICANT: Heston, Warren D.W.
 ; APPLICANT: Fair, William R.
 ; APPLICANT: Overfelli, Quathek
 ; APPLICANT: Pinto, John
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 1769/41426-G
 ; CURRENT APPLICATION NUMBER: US/08/705,477E

; CURRENT FILING DATE: 1996-08-29
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 101
 ; LENGTH: 693
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-08-705-477E-101

Query Match 97.9%; Score 2281; DB 4; Length 693;
 Best Local Similarity 97.7%; Pred. No. 7.5e-214;
 Matches 432; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGSAPPDSSMRSLKSYVNGPGFTGNFSTOKYKMHISTNEVTRIYNYIGTLRGAVP 60
 DB 252 MGSAPPDSSMRSLKPYVNGPGFTGNFSTOKYKMHISTNEVTRIYNYIGTLRGAVP 311
 QY 61 DRYVILGHRDVSFVGIDPQSGAAVYHETVRSFGTLKKGWRPRTTILFASMDAEFGL 120
 DB 312 DRYVILGHRDVSFVGIDPQSGAAVYHETVRSFGTLKKGWRPRTTILFASMDAEFGL 371
 QY 121 LGSTEMADNSRLIOERGVAIYNADSSIEGNYTLRVCTPLMYSLYNLTRELKSPDEGF 180
 DB 372 LGSTEMADNSRLIOERGVAIYNADSSIEGNYTLRVCTPLMYSLYNLTRELKSPDEGF 431
 QY 181 EGKSLYESWTKKSPSPFSGMPRIKSLGSGNDFEVFORGLIASGRARYTKNMETNFKFSG 240
 DB 432 EGKSLYESWTKKSPSPFSGMPRIKSLGSGNDFEVFORGLIASGRARYTKNMETNFKFSG 491
 QY 241 YPLHYSYETVELVEKRYDPMFKYHLTVAOVRGGMVELANSIVLPDCRDYAVVLKRYA 300
 DB 492 YPLHYSYETVELVEKRYDPMFKYHLTVAOVRGGMVELANSIVLPDCRDYAVVLKRYA 551
 QY 301 DKYINIMKHPQEMKTYSLSPDSLFSVKNFTETASKFSERLODFDSNPILLRMNDOL 360
 DB 552 DKYISIMKHPQEMKTYSLSPDSLFSVKNFTETASKFSERLODFDSNPILLRMNDOL 611
 QY 361 MFLERAFIDPLGIDPRPFYRHVYIAPSSHNKYAGESPGIYDALFIDIESKVPKANGDV 420
 DB 612 MFLERAFIDPLGIDPRPFYRHVYIAPSSHNKYAGESPGIYDALFIDIESKVPKANGDV 671
 QY 421 KROIYVAFTVOAAAEFTLSEYA 442
 DB 672 KROIYVAFTVOAAAEFTLSEYA 693

RESULT 8
 ; US-08-547-197-1
 ; Sequence 1, Application US/08547197
 ; Patent No. 5691157
 ; GENERAL INFORMATION:

; APPLICANT: Gong, Joseph K.
 ; APPLICANT: Glomski, Chester A.
 ; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
 ; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMETRIC AGENTS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 14603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/547,197
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Rogalsky, Peter
 ; REGISTRATION NUMBER: 38,601
 ; REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (716) 263-1634
 ; TELEFAX: (716) 263-1600
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 622 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-547-197-1

Query Match 19.1%; Score 445.5; DB 1; Length 622;
 Best Local Similarity 26.0%; Pred. No. 1.2e-34;
 Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;

QY 1 MGSAPPDSSMRSLKSYVNGPGFTGNFSTOKYKMHISTNEVTRIYNYIGTLRGAVP 56
 DB 211 MEGNCPSPWNIDSSCK--LELSQN-----QNVKLVNNVYLKETRLINIFYIKG 257
 QY 57 AVEPDYVILGHRDVSFVGIDPQSGAAVYHETVRSFG--TLKKGWRPRTTILFASMDA 115
 DB 258 YEEPDYVIVGAQRDAMGPGVAKSSVGTGLLKLQVFSMDISKDGRPSRSLIFASMTA 317
 QY 116 EEFGLSTEMADNSRLIOERGVAIYNADSSIEGNTLTVDCPLMYSLYNLTRELKLS 175
 DB 318 GDYGAVPTPEMLEYLSLHLKAFYIINDKLVIGTNSFNKVASAPSLTYTLGKIMQDVKH 377
 QY 176 PDEGFEEKSLY--ESWTKKSPSPFSGMPRIKSLGSGNDFEVFORGLIASGRARYTKNW 233
 DB 378 P---IDKYLXLRNNSMJSK-----IEELSDNNAFPFLATYSGIRAVSPCFED- 422
 QY 234 EYKFSQPLHYHSYETVELVEKRYDPMFKYHLTVAOVRGGMVELANSIVLPDCRDY 293
 DB 423 ---EDYPLGTLDYELLIOKVPOLDNOMVRAAIVAGOFIKTLNHDIELTLDYBMYN 477
 QY 294 VVLKRYADKIYINIMKHPQEMKTYSLSPDSLFSVKNFTETASKFSERLODFDSNPILL 353
 DB 478 SKLLSPKDLNQK---ADIKDMLSLQWLYSARGYFRATSLUTDFHNAEETNRFV 533
 QY 354 RMMNDOLMFLERAFIDPLGIDPRPFYRHVYIAPSSHN-----KYAGESFPGIYDALF 405
 DB 534 REINDRIMKYVHLSYVSPRESRPHIFMGSSHTLSALVENLRLRQKNITAFNFTL 593
 QY 406 DIESKVPKANGDVKKROIYVAFTVOAAAEFTLS 439
 DB 594 -----RQDLALATWTIOGVANALS 612

RESULT 9
 ; US-08-957-940-1
 ; Sequence 1, Application US/08957940
 ; Patent No. 6132981
 ; GENERAL INFORMATION:

; APPLICANT: Gong, Joseph K.
 ; APPLICANT: Glomski, Chester A.
 ; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
 ; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMETRIC AGENTS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 ; STREET: Clinton Square, P.O. Box 1051
 ; CITY: Rochester
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 14603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,940
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-957-940-1

Query Match 19.1%; Score 445.5; DB 3; Length 622;
Best Local Similarity 26.0%; Pred. No. 1.2e-34;
Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;

QY 1 MGSAPP---DSWRSGLKVSANVGPCTGNSFQKVMHISTEVRINVTGLG 56
DB 211 MGNCPSPSNIDSSCK--LELSON-----QNVALLVNNVAKERILNIEGVIG 257
QY 57 AVEPDRVYLGGHRSWVGIGIDPOSGAAVHEIVRSFG-TLKEGMRPRRTILFASWDA 115
DB 258 YEERPRVYVGAORAMGPGVAKSSVGTGLLKLQVFSDMISKDGFSPRSIIIFASMTA 317
QY 116 EEEGLLGSTWMAEDNSRLQERGVAYINADSSIEGNTLRVDCPTLMYSLVNTKELKS 175
DB 318 GDYGVANGPEMELEGYLSHLKAFYIINDKAVLGNFKVASPLLYLTMGKIMODVAH 377
QY 176 PDEGREGKSLY--ESWTKKSPSPFSGMRISKLSGNDPEVFFORLGIASGRARYTKNM 233
DB 378 P--IDGKLYRNSNMISK-----IEELSLDNAAPFLAVSGIPAVSFCECD- 422
QY 234 EFNKSGYPLHYSVETVLEKFDPMKHYIAQVGVGNVFEELANSIVLPFCRDYA 293
DB 423 -----EDPYLGTKLDYELILQKVQDLNQWRTAAEVAAGOFILKILHDIELTLDYEMYN 477
QY 294 VVLRKYADKIYINISMKHPQEMKTYSLSPDLSFSAVNFEELASKFSERLQDPEKSNPIL 353
DB 478 SKLLSFMKDLNQF---ADIKDMGLSLQWLYSARGDYFRATSRKLTIDPHNAEKINRYVA 533
QY 354 RMANQMLERAFIDPLGLPDRPFYRHVAYPSSHN-----KYASESPFGIYDALF 405
DB 534 REINRIMKVEHYELFSPYVSPRESPEFHIFMGSGHTLSALVENLRLRQKNITAFNETLF 593
QY 406 DIESKVDPSKAMGDVKKQISVAAPFYQAAAEFLS 439
DB 594 -----RNDLALATWTIQQVANAALS 612

RESULT 10
US-08-547-197-2
Sequence 2, Application US/08547197
Patent No. 5691157
GENERAL INFORMATION:
APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-547-197-2

Query Match 18.2%; Score 425; DB 1; Length 760;
Best Local Similarity 26.5%; Pred. No. 1.6e-32;
Matches 110; Conservative 93; Mismatches 172; Indels 40; Gaps 11;

QY 31 TOKVMKHISTEVRINVTGLRGAVPEPDRVYLGGHRSWVGIGIDPOSGAAVHEHT 90
DB 370 SKAVKLYVSNVLAKEIKILNIEFVIGFVPEPDHYVGAORAMGPGAAKSGVGTALLKL 429
QY 91 VRSFGTL-KKEGMRPRRTILFASWDAEEFGLLGSTWMAEDNSRLQERGVAYINADSSIE 149
DB 430 AQMFSDMYLKDGFQSPRSIIIFASWSAGDGSVGATMELEGYLSHLKAFYIINDKAVL 489
QY 150 GNYTLRVDCPTLMYSLVNTKELSPDEGFEKSLYE--SWTKKSPSPFSGMRISKL 207
DB 490 GTSNFKVSASPLLYLILEXTMQNVKHP--VTGQFLYDSSMAASK-----VERL 535
QY 208 GSGNDEVEFFORLGIASGRARYTKNMETNKFSGYPLHYSVETV-ELVEKFDPMKHYHL 266
DB 536 TLDNNAFPFLAVSGIPAVSFCECD-----IDPYLGTKLMDTYKELIERIPE-LNKAR 588
QY 267 TVAQVRCGVNFEELANSIVLPFCRDYAVVLRKYADKIYINISMKHPQEMKTYSLSPDLS 326
DB 589 AAEEVAGQFVILKTHDVELINDYERYNSQLSFDVRLNG---YRADIKEMGLSLQWLYS 644
QY 327 AVKNFTEASKRSERLQDPEKSNPILRLMNMNQMLERAFIDPLGLDPRFVRYIYAP 386
DB 645 ARGDFFRATSRITTDTEGNAEKTDPRVKKLNDRVARVEHPLSPVVSRESPEFRHVEWGS 704
QY 387 SSHNKYAGESPFGIYDALFDEIESKVDPSKAMGDV--KKQISVAAPFYQAAAEFLS 439
DB 705 GSH-----TLPAL--LENLKLKRONNGAFNETIFRNDLALATYTIQGAANAALS 750

RESULT 11
US-08-957-940-2
Sequence 2, Application US/08957940
Patent No. 6132981
GENERAL INFORMATION:
APPLICANT: Gong, Joseph K.
APPLICANT: Glomski, Chester A.
TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
NUMBER OF SEQUENCES: 2

```

1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
3 STREET: Clinton Square, P.O. Box 1051
4 CITY: Rochester
5 STATE: New York
6 COUNTRY: U.S.A.
7 ZIP: 14603
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patent Release #1.0, Version #1.30
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/957,940
16 FILING DATE:
17 CLASSIFICATION:
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US/08/547,197
20 FILING DATE:
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Rogalsky, Peter
23 REGISTRATION NUMBER: 38,601
24 REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (716) 263-1634
27 TELEFAX: (716) 263-1600
28 INFORMATION FOR SEQ ID NO: 2:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 760 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35
36 US-08-957-940-2

```

[illegible]

```

APPLICANT: Alexander Blinkovsky
APPLICANT: Kimberly Brown
APPLICANT: Elizabeth Gollightly
APPLICANT: Tony Byun
APPLICANT: Thomas Mathiasen
APPLICANT: Lene V. Korod
APPLICANT: Mikio Fujii
APPLICANT: Chigusa Shizuoka
TITLE OF INVENTION: Methods For Producing Protein
TITLE OF INVENTION: Hydrolysates
FILE REFERENCE: 5253.500-US
CURRENT APPLICATION NUMBER: US/09/079,955A
CURRENT FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 496
TYPE: PRM
ORGANISM: Aspergillus oryzae
US-09-079-955-2

```

```

OY      5.7%; Score 133.5; DB 4; Length 496;
Query Match 25.5%; Pred. No. 0.00024;
Best Local Similarity 25.5%;
Matches 51; Conservative 29; Mismatches 87; Indels 33; Gaps 9;

OY      34 VKMHISTNEVTRIYNIGTLRGAVEPDRYVILGHRDSWVG-GIDPQGAAYHETVR 92
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      214 VDLVWDSKQENRTTYNVAQTKGG-DPNVVALGCHTDSVEAGPGLN-DDSGIISNLVY 271
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

OY      93 SFGTLKKGWMPRTTILFASWDAEEFGILGSTEMEDMSRLLOEGVAYINADSSIEGNY 152
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      272 AKALIQ--YVKNAVRFLFTAEFFGLGSYVSHLNATELKRILTLNFDMTASPNY 328
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

OY      153 TLRYVDCPTPLMSLYN---LTKELKSPDEGEKSLYSEWTKKSPSP---EFGMPRIS 205
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      329 AL-----MIYDGDGSAFNQSGPAGSAQIEKLFEDYDIDPLPHIQFQGR----- 374
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

OY      206 KLGSGNDFEYVFFQRLGIASG 225
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      375 -----SDYEAFILN-GIPSG 388
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 13
US-09-330-095-1
; Sequence 1, Application US/09330095
; Patent No. 6127161
; GENERAL INFORMATION:
; APPLICANT: Kikkoman Corporation
; TITLE OF INVENTION: Leucine Aminopeptidase Gene, Recombinant DNA, and
; TITLE OF INVENTION: Process for Producing Leucine Aminopeptidase
; FILE REFERENCE: PH-622
; CURRENT APPLICATION NUMBER: US/09/330,095
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: JP-164611/1998
; EARLIER FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Aspergillus sojae
US-09-330-095-1

Query Match 5.6%; Score 131.5; DB 3; Length 481;
Best Local Similarity 25.5%; Pred. No. 0.00036;
Matches 51; Conservative 29; Mismatches 87; Indels 33; Gaps 9;

OY      34 VKMHISTNEVTRIYNIGTLRGAVEPDRYVILGHRDSWVG-GIDPQGAAYHETVR 92
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      199 VDLVWDSKQENRTTYNVAQTKGG-DPNVVALGCHTDSVEAGPGLN-DDSGIISNLVY 256
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

OY      93 SFGTLKKGWMPRTTILFASWDAEEFGILGSTEMEDMSRLLOEGVAYINADSSIEGNY 152
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

```

```
Db      257 AKALTO---XSVKNAVFLFWTAEEFGLLGSNTYVSHLNTLTKIKILYNFDMIASPNY 313
OY      153 TLKVDCTPLMYSLVYN---LTKEIKSPDEGEFEGKSLEYEWTKKSPSP---EFGMPRIS 205
Db      314 AL-----MIDYDGSASFNOSGASQAQIEKLFEDYDSDIDPHITQFDGR----- 359
OY      206 KLGSGNDEVEVFORLGIASG 225
Db      360 -----SDYEAFILN-GIPAG 373

RESULT 14
US-09-482-273-120
; Sequence 120, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (473)
; OTHER INFORMATION: xaa equals stop translation
US-09-482-273-120

Query Match      5.3%; Score 122.5; DB 4; Length 473;
Best Local Similarity 32.1%; Pred. No. 0.0027;
Matches 27; Conservative 18; Mismatches 34; Indels 5; Gaps 2;

OY      45 TRIYVIGTLRGAVEPRRYVILGHRDSWVF--GIDPQSGAAVYHETVRSFGTLKKEGW 102
Db      266 TDSFNTVAETGSKYPRQVVLVSGHLDSMDVGGAMDGDGGAFTSWE---ALSLIKDLGL 322
OY      103 RPRRTILFASWDAEEFGLLSTEW 126
Db      323 RPKRTLRLVLTWTAEEGGVGGAFOY 346

RESULT 15
US-09-252-991A-18292
; Sequence 18292, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; EARLIER FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18292
; LENGTH: 584
; TYPE: PRT
```

```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18292

Query Match      5.2%; Score 121.5; DB 4; Length 584;
Best Local Similarity 25.9%; Pred. No. 0.0047;
Matches 60; Conservative 41; Mismatches 84; Indels 47; Gaps 14;

OY      10 SWRGSILKY---SYNVGPGFTGNFSTQKVKH--IHSTNEVTRYLYNIG-TLRGAVEPRDRY 63
Db      284 SYEGGIPVIPATYDNGVAMS---QTPDLQLHLVADVVRKKTETYNVVAETRRG--NPNNV 338
OY      64 VILGGRDSWVFGG---IDPQSGAAVYHETVRSFGTLKKEGWRPRRTILFASWDAEEFGL 120
Db      339 VMVGAHLDS-VFEGSPGINDSGSAAQLE---MAVILAKA-LPVNKRVPAMWGAEEBAGL 392
OY      121 LGSTEWAEKDSRLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVYNLTKEIKSPDEGF 180
Db      393 VGSTHYVQNLPAPEKKKIKAYLNFDMIGSPNFG-----NFTYDGDGSDPGL 438
OY      181 EG-----KSLVESWTKKSPSPFEGMPRIHSKSGNDPEVFORLGIASG 225
Db      439 QGPPGSAATIRLFEAYFRLR-GQOSEG---TEIDFRSDYAEFFNS-GIAFG 484
```

Search completed: October 4, 2003, 23:26:47
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 23:09:12 ; Search time 39 Seconds
(without alignments)
1089.912 Million cell updates/sec

Title: US-09-973-382C-2
Perfect score: 2329
Sequence: 1 MGSAAPPDSSMRGSLKVSYN.....QISVAFAFTVQAAETLSEVA 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2288	98.2	750	2	A56881	prostate-specific
2	631.5	27.1	751	2	T30154	hypothetical prote
3	579	24.9	703	2	T47631	peptidase-like pro
4	545.5	23.4	1483	2	T19751	hypothetical prote
5	445.5	19.1	622	2	A34549	transferrin recept
6	435	18.7	763	1	S29548	transferrin recept
7	426	18.3	760	1	JXHU	transferrin recept
8	424.5	18.2	757	2	A48592	transferrin recept
9	413.5	17.6	776	1	JH0570	transferrin recept
10	399	17.1	811	2	S57149	probable membrane
11	355	15.2	794	2	T40289	hypothetical prote
12	252	10.8	280	2	E85075	probable peptidase
13	240.5	10.3	809	2	S67153	probable membrane
14	179.5	7.7	783	2	S67158	secretory protein
15	173	7.4	529	2	G82159	hypothetical prote
16	157	6.7	467	2	G87564	aminopeptidase, pr
17	152.5	6.5	430	2	A87634	peptidase, M20/M25
18	148	6.4	501	2	G82414	aminopeptidase VCA
19	140.5	6.0	284	2	S66427	aminopeptidase (EC
20	139.5	5.7	374	2	S24314	bacterial leucyl a
21	133	5.7	374	2	S66969	hypothetical prote
22	130.5	5.6	500	2	H70629	probable AMINOPEPT
23	126.5	5.4	493	2	T46974	leucyl aminopeptid
24	121.5	5.2	536	2	B83378	probable aminopept
25	118.5	5.1	455	2	S39653	aminopeptidase hom
26	117	5.0	609	2	JC7819	metalloprotease
27	116	5.0	893	2	T18271	hypothetical prote
28	116	5.0	1123	2	T18270	hypothetical prote
29	113.5	4.9	647	2	A83606	hypothetical prote

30	113	4.9	468	2	F87359	leucine aminopepti
31	112	4.8	411	2	B90701	allantoate amidohy
32	112	4.8	411	2	E85551	probable hydantoin
33	111	4.8	537	2	A54134	aminopeptidase y (
34	108	4.6	411	1	C64783	probable N-cardamy
35	107.5	4.6	488	2	A87569	peptidase M20/M25/
36	107.5	4.6	1447	2	S63669	UDPglucose-glycopr
37	107	4.6	980	2	T24556	hypothetical prote
38	106.5	4.6	449	2	H97249	protein containing
39	106.5	4.6	571	2	H87600	hypothetical prote
40	106	4.6	1481	2	S28669	pullulanase (EC 3.
41	105	4.5	2957	2	T33152	hypothetical prote
42	103	4.4	816	2	C83424	assimilatory nitri
43	103	4.4	855	2	A71223	hypothetical prote
44	102.5	4.4	759	2	J01045	aryphorin precurs
45	101.5	4.4	704	2	T01772	hypothetical prote

ALIGNMENTS

RESULT 1
A56881
prostate-specific membrane antigen - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000
C/Accession: A56881
R/Israeli, R.S.; Powell, C.T.; Fair, W.R.; Heston, W.D.
Cancer Res. 53, 227-230, 1993
A/Title: Molecular cloning of a complementary DNA encoding a prostate-specific membra
A/Reference number: A56881; MUID:93113576; PMID:8417812
A/Accession: A56881
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-750 <ISR>
A/Cross-references: GB:M99487; NID:q190663; PIDN:AAA60209.1; PID:q190664
A/Experimental source: Prostatic carcinoma cell line LNCaP
A/Note: sequence extracted from NCBI backbone (NCBIN:121724, NCBI:P.121725)
C/Superfamily: transferrin receptor
C/Keywords: surface antigen; transmembrane protein

Query Match	Score	2288	DB 2	Length	750
Best Local Similarity	98.0%	Pred. No.	1.8e-163		
Matches	433	Conservative	6	Mismatches	3
				Indels	0
				Gaps	0
QY	1	MGSAAPPDSSMRGSLKVSYNVGVGFTGNFSTOKVKKHISTNEVTRIVVIGTLRGAVBP	60		
DB	309	MGSAAPPDSSMRGSLKVPYVNGPFTGNFSTOKVKKHISTNEVTRIVVIGTLRGAVBP	368		
QY	61	DRVYVILGHRDMSVFGCIPDQSGAAVYHETVRSFGTLKKEGMRPRRTILFASMDAEFGI	120		
DB	369	DRVYVILGHRDMSVFGCIPDQSGAAVYHETVRSFGTLKKEGMRPRRTILFASMDAEFGI	428		
QY	121	LGSTEWAEADNSRLLOERGAAYINADSSIEGNTYLRYDCTPLMYSLVYNTLKELSPDEGF	180		
DB	429	LGSTEWAEADNSRLLOERGAAYINADSSIEGNTYLRYDCTPLMYSLVYNTLKELSPDEGF	488		
QY	181	EGKSLEYESTTKKSPSPFSGMPRIKLSGNDPFEVFFQRLGASGARATYTKMNETKFSG	240		
DB	489	EGKSLEYESTTKKSPSPFSGMPRIKLSGNDPFEVFFQRLGASGARATYTKMNETKFSG	548		
QY	241	YPLVHSVYETVELVEKFDYDPMFKYHLTLVAOVRGMYEELANSIVLPFDDCRDAVAVLRKA	300		
DB	549	YPLVHSVYETVELVEKFDYDPMFKYHLTLVAOVRGMYEELANSIVLPFDDCRDAVAVLRKA	608		
QY	301	DKTYINSMKHPQEMKTYSLFSDSLFSAVKNFTETLAKSFSERLQDPDKSNPILLRMNNDOL	360		
DB	609	DKTYINSMKHPQEMKTYSLFSDSLFSAVKNFTETLAKSFSERLQDPDKSNPILLRMNNDOL	668		
QY	361	MFLEKAFIDPLGIDPDRPFRHRYVLAASSHNKTAGESFPGIYDALFPIESKVDPSKMGCV	420		
DB	669	MFLEKAFIDPLGIDPDRPFRHRYVLAASSHNKTAGESFPGIYDALFPIESKVDPSKMGCV	728		


```

Db      320 MKGDA-VNADEFGKLNIVRYGPGILNN---OKLRVYAEENEERSVIYVELLSRLNLF 375
Oy      45 TRIVAVIGTLRCAVPPDRYVILGHRDSVFGGIDPOGAAVHETVRSFGTLKKE-GWR 103
Db      376 RQIONMGKIKSGSPDDKFLVSNHYDAWTYGAVNSGTSFLLVESRLKQYQONTGMI 435
Oy      104 PARTLLFASWDAEEFGILGSTEMAEDNSRLLOERGAAYINADSSIEGNTYLLVDCPTLMY 163
Db      436 PARSLIFAMDMDEEGLIGLSTFEAEERYRLQLMRRVAVYINMD-LIGGNOTLLGLNSPIYA 494
Oy      164 SLVYNLTRELKSPD--EGFEG-KSLYESWTKKSPSPFGSMRISKL-GSGNDFEYFQR 219
Db      495 NVLRSAANAANVEQNPFTMEQGRKTLDSWKYAPSKNNNSRTHPYORIPAGSGDHLPEFDY 554
Oy      220 LGI-----ASGRARYTNMETNKFSGPLVHSYETELVEKFKFDPMFKHLYVAQVR 272
Db      555 LGPIVFFITSSLDAPPT-----YPLVHTIYETPYLLEIMDPCKYHKAKIAGMF 604
Oy      273 GGMVEFLANSIYLPDPCRDYAVVLRKRYADKIYNISMKHPQEM-KTYSL--SPDSLSAVK 329
Db      605 IECILKFTMSKTLPLDNL-----MDSIFEYLPKLEDRINKLMTICTKTDYLLDAOK 658
Oy      330 NFETLASFSERLQDPKSN-----PILLRM-MNDQLMFLERAFIDPLGPDPRFYRH 381
Db      659 OFKLQKTYLELSEIYQRNYSKLEELPFGSRVDINNRLIEFEKCFINPHGAIGNQARH 718
Oy      382 VYIYASSHNKYGSEFPGLYDALFDIESKVDPSKMGDYKRQISVAALFYQAA 434
Db      719 VLEHSPDMWYDGDALISQVHDLISKISNSTD-SKEGLKSLROLAKEIALVNVA 770

```

RESULT 5

```

transferrin receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C:Accession: A34549
R:Roberts, K.P.; Griswold, M.D.
Mol. Endocrinol. 4, 531-542, 1990
A:Title: Characterization of rat transferrin receptor cDNA: the regulation of transferrin
A:Reference number: A34549; MUID:91125359; PMID:2126342
A:Status: preliminary
A:Accession: A34549
A:Residues: 1-622 <ROB>
A:Molecule type: mRNA
A:Cross-references: GB:M56040; NID:9207463; PIDN:AAA42273.1; PID:9207464
C:Superfamily: transferrin receptor
C:Keywords: receptor; transmembrane protein

```

```

Query Match      19.1%: Score 445.5; DB 2: Length 622;
Best Local Similarity 26.0%: Pred. No. 1.9e-25;
Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;

Oy      1 MGSGAP-----DSWRGSLKSYNVNGPFTGNFSTOKVAMHISTNEVRIYVIGTLRG 56
Db      211 MGCNCPSPMNISSCK--LELSQN-----QNVKLYNNVLAKEIRILNIGVIKG 257
Oy      57 AVEPRRIYVLGHRDSWVFGGIDPOGAAVHETVRSFG-TLKGSRPRRTILLASWDA 115
Db      258 YEPRRIYVAGQORAWMGVAKSSVGTGLLKLKLAQVSDMTSKDGFRRPSRSIIIRASWTA 317
Oy      116 BEFGILGSTEMAEDNSRLLOERGAAYINADSSIEGNTYLLVDCPTLMYSLVYNLTRELKKS 175
Db      318 GDYGVAGPEWLEGLSLSLHLKAFYIINDKVVLTGTSNEKVASPLTLTKKIMQDVAKH 377
Oy      176 PDEGEGKSLY--ESWTKKSPSPFGSMRISKLSGNDFEYFQRLGIASGRARYTKNW 233
Db      378 P---IDGKLYLNNSMWISK-----IELSLDNNAAPFLAYSGIPAVSFCED- 422
Oy      234 EYNKSGIPLVHSYETELVEKFKFDPMFKHLYVAQVRGGMVFLANSIYLPDPCRDYA 293
Db      423 -----EDYPVLTGKLDYELIQLQKVPOLNQMWRTAAEAVAGQFLIKLTHDIELTLEYEMYN 477

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Oy      294 VVLRKYADKIYNISMKHPQEMKTSLSPEDSLFSAVKNFTELASKESERLODPKSNPILL 353
Db      478 SKLLSFMKDLNFK-----ADIKMDGLSLQWLYXSAAGDYRRAISRLLTDPHNAEKNNRFWM 533
Oy      354 RMNDQLMFLERAFIDPLGPDPRPFYRHVYAPSSHN-----KYAGESPGLYDALF 405
Db      534 REINDRIMKVEHYHFLSPYSPRESPEFRHIFMGSGSHTLALVENLRLOKNITAFNETLF 593
Oy      406 DIESKVDPSKMGDYKRQISVAALFYQAAETLS 439
Db      594 -----RNDLALATWTIQQVANAALS 612

```

RESULT 6

```

transferrin receptor - mouse
N:Alternate names: CD71; p90
N:Contains: 85K serum transferrin receptor
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29548; A26735; D24550; I49662
R:RitowdrIDGE, I.S.; Domingo, D.L.; Thomas, M.L.; Chain, A.
submitted to the EMBL Data Library, January 1991
A:Reference number: S29548
A:Accession: S29548
A:Status: preliminary

```

```

A:Molecule type: mRNA
A:Residues: 1-763 <PRO>
A:Cross-references: EMBL:X57349; NID:954914; PIDN:CAA40624.1; PID:954915
R:Rothenberger, S.; Iacopetta, B.J.; Kuhn, L.C.
Cell 49, 423-431, 1987
A:Title: Endocytosis of the transferrin receptor requires the cytoplasmic domain but
A:Reference number: A26735; MUID:87187639; PMID:3568132
A:Accession: A26735

```

```

A:Molecule type: protein
A:Residues: 1-82 <ROT>
R:Grego, B.; Van Driel, I.R.; Stearne, P.A.; Goding, J.W.
Eur. J. Biochem. 148, 485-491, 1985
A:Reference number: A24550; MUID:85203852; PMID:2986964
A:Accession: D24550
A:Molecule type: protein
A:Residues: 7-19;158-175,'X',177-179;'DESL','AV',189,'IEN',193,'FXEF',195;196,197-208
A:Note: these tryptic fragments have been ordered by homology with the human sequence
J. Immunol. 134, 3474-3479, 1985
A:Title: CDNA cloning of the murine transferrin receptor: Sequence of trans-membrane
A:Reference number: I49662; MUID:85159078; PMID:2984291
A:Accession: I49662
A:Status: translated from GB/EMBL/DBJ

```

```

A:Molecule type: mRNA
A:Residues: 'AL',27-149,'O',151-301 <RES>
A:Cross-references: GB:M29618; NID:9193272; PIDN:AAA37616.1; PID:9193273
C:Comment: This transmembrane glycoprotein exists as a dimer of similar or identical
ty acyl groups. The amino end of each chain lies within the cytoplasm and a stop-tra
embrane, may also serve as an internal signal sequence.
C:Comment: The expression of this receptor, involved in the regulation of cell growth
C:Function:
A:Description: mediates cell iron uptake by binding, internalizing, and recycling the
C:Superfamily: transferrin receptor
C:Keywords: glycoprotein; iron transport; receptor; transmembrane protein
F:1-57/Domain: intracellular #status predicted <INT>
F:58-61/Region: stop-transfer sequence
F:62-89/Domain: transmembrane #status predicted <TMS>
F:89-763/Domain: extracellular #status predicted <EXT>
F:101-763/Product: 85K serum transferrin receptor #status predicted <MAT>
F:253,319,730/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match      18.7%: Score 435; DB 1: Length 763;
Best Local Similarity 26.7%: Pred. No. 1.5e-24;
Matches 123; Conservative 88; Mismatches 171; Indels 78; Gaps 14;

Oy      1 MGSGAP-----DSWRGSLKSYNVNGPFTGNFSTOKVAMHISTNEVRIYVIGTLRG 56

```

```

Db      351  MEGSCPAPAMINDSCK--LELSQN-----QNKVLTKVKNLKERILLINIFGVITG  397
Qy      57   AVEEDRYVILIGHNDSWFVGIDPQS--GAAVHEHYASFG-TLKEGEMRRRIITLFASW  113
           |||||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     398  YEEDDRYVVAQXDA-LGAGVAAKSSVGTULLKLQAFSDMISKDOFRRSRIITFSW  456
Qy     114  DAEERGLIGSTEWAEADNSRLLOERGVAIYANDSSIEGNYTLRVCDTPLMYSLVYNLREL  173
           ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     457  TNGDFGAGATEWLEGYLSLHLKAFYIINDKVVILGTSNFKVASPILLYTLKMGIMQDV  516
Qy     174  KSPDEGEGKSL--ESWTKRSPSEFGSMRISKLSGNGPEVFPQGLIASGARATK  231
           ||::: |||||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     517  KHP--VDGKSLYRDSMWISK-----VEKLSFDMAAPFLAYSGIAPVSCFCE  562
Qy     232  NMETNKFSGYLYSHVSYETELVEKFYDPMFKYHLTVQVNGWMEFLANSIVLPDORD  291
           ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     563  D-----ADYELGLTRDITPALTOKVPQLQMWRTALEVAGQLITKLTHDELVLDEM  616
Qy     292  YAVVLRYKADKIYINISMKHPQEMKT---YSLSPDLSAKNKFTIASKESERLODDX  347
           ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     617  YNSKLSLF-----MKDLNQFKTDIRDMGLSLQWLIVSANGDYFRATSRLLTDPHNMEK  668
Qy     348  SNPILLRMANDQLFLERAFIDPLGLPDRPFYRHVITYAPSSH-----KYAGESFPG  399
           ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     669  TNRVYREINIRIMKVEHYHFLSPYSPRESPEFHIFMGSGHSLTALVENIKLRQKNITA  728
Qy     400  IYDALFDIESKVDPSKAMGDYKROIISVAATVQAAAEFLS  439
           ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
Db     729  FNETLTF-----RNOIALATATWIIQGVANLS  753

```

RESULT 7

UJHU

transferrin receptor - human

N:Alternate names: CD71; p90

N:Contains: 85k serum transferrin receptor

C:Species: Homo sapiens (man)

C:Date: 25-Feb-1985 #sequence-revision 25-Feb-1985 #text-change 22-Jun-1999

C:Accession: A93343; A90856; A36597; S54327; S09039; A03259

R:Schneider, C.; Owen, M.J.; Banville, D.; Williams, J.G.

Nature 311, 675-678, 1984

A:Title: Primary structure of human transferrin receptor deduced from the mRNA sequence.

A:Reference number: A93343; MUID:85012743; PMID:6090955

A:Accession: A93343

A:Molecule type: mRNA

A:Residues: 1-760 <SCH>

A:Cross-references: GB:X01060; NID:g37432; PIDN:CAA25527.1; PID:g37433

R:McLelland, A.; Kuhn, L.C.; Ruddle, F.H.

Cell 39, 267-274, 1984

A:Title: The human transferrin receptor gene: genomic organization, and the complete primary structure.

A:Reference number: A90856; MUID:85046936; PMID:6094009

A:Accession: A90856

A:Molecule type: mRNA

A:Residues: 1-760 <MC>

A:Cross-references: GB:M11507; NID:g339515; PIDN:AAA61153.1; PID:g339516

R:Shih, Y.J.; Baynes, R.D.; Hudson, B.G.; Flowers, C.H.; Skine, B.S.; Cook, J.D.

J. Biol. Chem. 265, 19077-19081, 1990

A:Title: Serum transferrin receptor is a truncated form of tissue receptor.

A:Reference number: A36597; MUID:91035436; PMID:2229063

A:Accession: A36597

A:Molecule type: protein

A:Residues: 101-103, 'X', 105-108, 'X', 110-119 <SH>

A:Experimental source: serum

R:Coppolino, M.; Migliorini, M.; Argraves, W.S.; Dedhar, S.

Biochem. J. 306, 129-134, 1995

A:Title: Identification of a novel form of the alpha(3) integrin subunit: covalent association with alpha(5) integrin subunit.

A:Reference number: S54327; MUID:95169043; PMID:7864799

A:Accession: S54327

A:Molecule type: protein

A:Residues: 288-302, 694-708, 721-730 <COP>

R:Alvarez, E.; Girones, N.; Davis, R.J.

Biochem. J. 267, 31-35, 1990

A:Title: A point mutation in the cytoplasmic domain of the transferrin receptor inhibits its function
A:Reference number: 509039; MUID:90226335; PMID:2327986
A:Accession: 509039
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-19, 'C', 21-61 <AT>
A:Note: mutant defective in endocytosis
C:Comment: This transmembrane glycoprotein exists as a dimer of similar or identical ty acyl groups. The amino end of each chain lies within the cytoplasm and a stop-transfer, may also serve as an internal signal sequence.
C:Comment: The expression of this receptor, involved in the regulation of cell growth.
C:Genetics:
A:Gene: GDB:TFRC
A:Cross-references: GDB:120433; OMIM:190010
A:Map position: 3q26.2-3q26.2
C:Function:
A:Description: mediates cell iron uptake by binding, internalizing, and recycling the C:Superfamily: transferrin receptor
C:Keywords: glycoprotein; iron transport; receptor; transmembrane protein
F:1-57/Domain: intracellular #status predicted <INT>
F:20-24/Region: tyrosine-based endosomal/Lysosomal sorting signal
F:58-61/Region: stop-transfer sequence
F:62-89/Domain: transmembrane #status predicted <TMS>
F:89-760/Domain: extracellular #status predicted <EXT>
F:101-760/Product: 85k serum transferrin receptor #status predicted <M>
F:251,317,727/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	18.38;	Score 426;	DB 1;	Length 760;
Best Local Similarity	26.58;	Pred. No. 7.2e-24;		
Matches 110;	Conservative 94;	Mismatches 171;	Indels 40;	Gaps 11;

OY 31 IQAKMHHSINETRIYNYIGTLRGAVEDPRYVILGGHDSWVFGSIDQSAAYVHET 90
 Db 370 SKNVKLTIVSNVLEKIKILINIFGVIKGFVEDPHYVVAQDAMPBGAKSGVGTALLKL 429
 OY 91 VRSEGTL-KKEGMERRTILFASWDAEEFGILGSTEAEEDNSRLJORGVAIYIADSSIE 149
 Db 430 AQMSDVMYKDGFPSPSIIIFASMSADDFGSGVGTATEGLSLSHLKAFYYINLDKAVL 489
 OY 150 GNYLRVDCIPPLAMSLVYNNLTKEKSPDEGEFGSKLYE--SWTKSPSPFESGMRLSKL 207
 Db 490 GTSNFKVASASPLVLTLEKTMQNVKHP--VTGGFLQDSMWASK-----VEKL 535
 OY 208 GSGNDFEVFQRLIASGRARYTKNMETNFKSGYPLHSHVYETV-ELVEKFYDPMKYHL 266
 Db 536 TLDMAAPPLAYSISIPAVSFCECD-----TDVPYLGTMIDYKELIERPE-LNKVAR 588
 OY 267 TVAOVRCGMVPELANSYVLPDCCRDYVYLKRYADKYINISMKHPQSKYISLSDSDFS 326
 Db 589 AAAYVAQOFYKTLHVDLNDYERYNSQLSFFRDL---NOYRAIDIKEMGSLQWLYS 644
 OY 327 AVKNETELASKEFSERLODFDKSNPILRMNDQMLFERAFIDPLGLPDRPFYRHVYAP 386
 Db 645 ARGGFPAITSLLTDFDPCNAEKTDFRYKKKLNDRMRYEHLHLSYVSPKSPFHVFMGS 704
 OY 387 SSNNKIVAGESPPGIYDALFDIESKYVDPSKAGDV--KRQISVAFTYQAAAETIS 439
 Db 705 GSH-----TLPAL--LENLKLRRQNNGAFNETLFRNQLALATWITQGANALS 750

RESULT 8
 A48592
 C:Species: Citicellus stuebeni (Chinese hamster)
 C:Date: 03-May-1994 #sequence.revision 03-May-1994 #text.change 20-Aug-1999
 C:Accession: A48592
 R:Collawn, J.F.: 161, A.; Domingo, D.; Fitch, M.; Hatton, S.; Trowbridge, I.S.
 J. Biol. Chem. 268, 21688-21692, 1993
 A:Title: YHRF is the conserved internalisation signal of the transferrin receptor,
 A:Reference number: A48592; MUID:94012745; PMID:8408022
 A:Accession: A48592
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-757 <COL>
 A:Cross-references: GB:119142; NID:q304528; PION:AAA03576.1; PID:q304529
 C:Superfamily: transferrin receptor
 C:Keywords: endocytosis; glycoprotein; transmembrane protein

Query Match 18.2%; Score 424.5; DB 2; Length 757;
 Best Local Similarity 24.9%; Pred. No. 9.3e-24;
 Matches 114; Conservative 88; Mismatches 182; Indels 73; Gaps 11;

QY 1 MGSAAPDDSSWRGSLKSYNVNPGFTGNFSTQVKMHISTNEVTRIYNVIGTLRGAVEP 60
 DB METNCP--SMNTDSCIKLESSQGINVLS-----VNNVLAKETRLNIFGYIKGEEP 336
 QY 61 DRYVILIGHRDSVFEIGIDPQGAAYVHETVRSFGLT-KKEGMRPRTTILFASWDAEEFG 119
 DB 397 DRIYVGAQORDAGPAAKSSVGTGLLKLAQAFSDMVSRGFGPKRSRITFASMSAGDFG 456
 QY 120 LIGSTMAEDNSRLDGRVAYINADSIIEGNTLVDCPLKYSLYVNLTKLSPDEG 179
 DB 457 AVGATEMLBEGYLSLHKAFETYINLDRVVLGTNFKVSAAPLLTYLLEKTMDQVRHP-- 513
 QY 180 FEKSLY--ESWTK-----SPSEFGMPRIISKSGNDEVEFQRLGIASGRA 227
 DB 514 IDGKPLRDSNMWISKVEDSLDAAAPFLAYSGIPAVSEFCNE----- 558
 QY 228 RTKKNETKFSQYPLVSHVYETELVEKFPYDMEKYHLTVAGVRCGMVFEANSLVLPF 287
 DB 559 -----DYPPLDNLDTYEKLQKVPOLNMKVRNAAEVAQGIKILKTHDIELNL 606
 QY 288 DCDYAVVLRKYADKLYNISIMKHPO---EMKTYSLSPDLSFSAVKNETELASFSERLD 344
 DB 607 D-----YDMYNNKILSFYKELNDFRAIDKAMGLQWLYLSKRGDFRATSLTDFPHN 659
 QY 345 FDKSNPILIRMMNDQMLELRAFDLPDRFPYRVHYAASSHNKYAGESPFIYDAL 404
 DB 660 AKKTNFVYREINNRIMKVEYHFLSPYSPRESPEFHIMGSSSHLTA-----LV 710
 QY 405 FDIKSVDPKAMGDV--KRQISVAFTYQAAAEITLS 439
 DB 711 ENLKLRQKNKSAFNETLFRNOLATWITQGVANALIS 747

RESULT 9

JH0570
 C:transferrin receptor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0570; S16855
 R:Gerhardt, E.M.; Chan, L.N.L.; Jing, S.; Qi, M.; Trowbridge, I.S.
 Gene 102, 249-254, 1991

A:Title: The cDNA sequence and primary structure of the chicken transferrin receptor.
 A:Reference number: JH0570; MUID:91340160; PMID:1874449
 A:Accession: JH0570
 A:Molecule type: mRNA
 A:Residues: 1-776 <GER>
 A:Cross-references: EMBL:X55348
 A:Note: 581 His and 736 Gln were also found as the result of polymorphism
 C:Comment: This protein mediates the endocytosis of the iron transferrin complex.
 C:Superfamily: transferrin receptor
 C:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transmembrane; coated-pit mediated internalization signal
 F:19-22/Region: coated-pit mediated internalization signal
 F:70-88/Domain: transmembrane #status predicted <TRK>
 F:23/Binding site: phosphate (Ser) (covalent) #status predicted
 F:70/Binding site: palmitate (Cys) (covalent) #status predicted
 F:261,326,391,738/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.8%; Score 413.5; DB 1; Length 776;
 Best Local Similarity 27.1%; Pred. No. 6.5e-23;
 Matches 121; Conservative 84; Mismatches 175; Indels 67; Gaps 14;

QY 11 WRG---SLKSYNVNPGFTGNFSTQVKMHISTNEVTRIYNVIGTLRGAVEPDRYVIG 67
 DB 367 WKGAHSCQV-----TKHESQIMVRLDVNNMSKKDKIINITGALIGFEEPRRYVIG 419

QY 68 GHRDSWVFEIGIDPQGAAYVHETVRSFGLT-KKEGMRPRTTILFASWDAEEFGLSTEW 126
 DB 420 AQRDSWPGVAKAGGTGAILLELAVRISDYLVKNRGYPRRSITIFASMSAGDYGVATTEW 479

QY 127 AEDNSRLDGRVAYINADSIIEGNTLVDCPLKYSLYVNLTKLSPDEGFEKSLY 186
 DB 480 LEGSAMLHAKAFETYISLDAPVLGASHVKISAPLLYMLGSIIMKGVKNP--AAVSSSLY 537

QY 187 E-----SWTK-----KSPSEFGMPRIISKSGNDEVEFQRLGIASGRARTKN 232
 DB 538 NRLGPDWVKAIVNPLGLDAAAPFLAYSGIPVLS-----FGFY----- 574

QY 233 METNKGYPVLYSHVYETELVEKFPYDMEKYHLTVAGVRCGMVFEANSLVLPFCRDY 292
 DB 575 ---NKDEYFELDTKGDTELENLKI-DNLDAALAAAEVAGQALRLTHDHELPLDIGRY 630

QY 293 AVVLRKYADKLYNISIMKHPOEMKTYSLSPDLSFSAVKNETELASFSERLDQDKSNPL 352
 DB 631 SEELLAYQEEF---LPYIKVERELGLTLDLFPAGDQFAVATLALRDIANDGGENRY 686

QY 353 LRMMNDQMLELRAFDLP-LGLPDRFPYRVHYAASSHNKYAGESPFIYDALFDIESKY 411
 DB 687 RRALNDRMKKVEYDFLSPYLSPKDVPF-RIIFPGKGPHTL---RSIVEHLQLLKTNRSSV 742

QY 412 DPSKAMGDVKKQISVAFTYQAAAEITL 438
 DB 743 DNLN-----LREQALATWITQKGAANAL 765

RESULT 10

S57149
 Probable membrane protein YJR126C - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein J2050

C:Species: Saccharomyces cerevisiae
 C:Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S57149
 R:Rose, M.; Koetter, P.; Entlian, K.D.
 Submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56848

A:Accession: S57149
 A:Molecule type: DNA
 A:Residues: 1-811 <ROS>
 A:Cross-references: EMBL:Z49626; NID:g1015854; PID:g1015855; GSPDB:GN00010; MIPS:YJR1
 A:Gene: MIPS:YJR126C
 A:Cross-references: SGD:S0003887
 A:Map position: 10R
 C:Keywords: transmembrane protein

Query Match 17.1%; Score 399; DB 2; Length 811;
 Best Local Similarity 27.5%; Pred. No. 8.4e-22;
 Matches 119; Conservative 77; Mismatches 164; Indels 72; Gaps 15;

QY 19 YNVGPG-----FTG-NFSTQVKMHISTNEVTRIYNVIGTLRGAVEPDRYVIG 69
 DB 387 FQIGPNSIKDRGSPGSSIDKXVHLNHELNYNKEKSSVAVSLPG-ITFGELITIGAH 445

QY 70 RDSWVFGGL-DPQGAAYVHETVRSFGLTKKEGMRPRTTILFASWDAEEFGLSGTEMAE 128
 DB 446 RSLSSSSAGANSALILELTAIRGMSKILKKGWPLRPIKILSWDGERSGGLSTDVAE 505

QY 129 DNSRLDGRVAYINADSIIEGNTLVDCPLKYSLYVNLTKLSPDEGFEKSLY 188
 DB 506 AHAALIRRALVYLMDNAISGT-NFCKKANDLDQVITEAAK--LTERNGHEDWSLEDDH 562

QY 189 WTKKSPSEFGMPRIISKSGNDEVEFQRLGIASGRARYTKMNETKFKSGYPLVH--S 246
 DB 563 W-----KYSNATISILDLGLSYTSFYHGLGVAAHQF-----NANDTSG-AVYHNS 610

QY 247 VYETELVEKFPYDMEKYHLTVAGVRCGMVFEANSLVLPFCRDYAVVLRKYADKTY-- 304
 DB 611 VFDSPTWLEKFTNSDYKLTNTWAMFVGLTTLMLSENELARFN-----THVYLLKITYNM 663

305 -----NISKMHQEMKTYSLSPDSLSAVKNFETASKFSERLQDPDKSNPLI----- 352
 664 YIAWHSNLSAIPQDDV-----NSLAKRYDLKAVTO--EDSIQDQNGILYKRCRE 716
 353 -----LRMNDQLMFLERAFIDPLGDPREFYRHVYADSSHNKIYGES 396
 717 ALPWAAFYKKIKYIKIQRNSKSKQIDQLFTHRGKLDREMKYSLAPSKFEGSVGEV 776
 397 FPGIYDALFDIE 408
 777 LFGIHEGLADID 788

RESULT 11
 740289
 hypotheical protein SPBC354.09c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: T40289
 C:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Gilbert, H.; Duesterhoeft, A.
 submitted to the EMBL Data Library, March 1998
 A:Reference number: 221918
 A:Accession: T40289
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-794 <MOO>
 A:Cross-references: EMBL:AL022071; PIDN:CAA17809.1; GSPDB:GN00067; SPDB:SPBC354.09c
 A:Experimental source: strain 972h-; cosmid c354
 C:Genetics:
 A:Gene: SPDB:SPBC354.09c
 A:Map position: 2
 C:Superfamily: secretory protein SSP134

Query Match 15.2%; Score 355; DB 2; Length 794;
 Best Local Similarity 25.0%; Pred. No. 1.6e-18;
 Matches 105; Conservative 80; Mismatches 185; Indels 50; Gaps 13;

11 WRGSLKSYNVGFGFNGFNSTQKVKMHIHSTNEVTRIVNYIGTLRGAVEDPRVYILGHR 70
 402 WTGS-KIS--SPGLEVNV-----LQDIEKQKIIINMAQIDG-YESDQILVGVAPR 448
 71 DSWVFGIDPQSGAAVYHETVRSFGLTKE-GMFRRTILFASWDAEFGILGSTEAE 129
 449 DSWCTGSDSSVGTSLIDVISTFANNAQDLSMKPRRTIYFASWDARQFMAIGSTEFLEY 508
 130 NSRLQERGAYITNADSSIGCNTLRYDCYPLMTSLVYNLTKEKSDDEGEKSLYESW 189
 509 WKSELEKAYAIIVDAVAVSGD-TFTARTVPGLEKKVIQRAFDVANEDEMKANITDDF 567
 190 TKKSPSPFSGMPRIKSLGSGNDEVFQRIASGRARYTKNMTNKGSGYPLYHSYE 249
 568 DYTSS-----DLTSFTLFGIPIVYNLAFTERNEPN--TTPFLGSCED 607
 250 TYELVEKFDPMFYKHLTVAVQRGVMEFLANSIVLPFCRDYAVVLRKYADKIYNISM 309
 608 TVSWIDTIGSEYWEAALGKIMSYLLIFLFLANDPVVPLDLEDEINGVEMLKRIPEIGA 667
 310 HPOEKTYSLSPDSLSAVKNFETASKFSERLQDP-----KSNPILLRMNDQLMFL 364
 668 NALDLARKINEESELLESLIRFEDEIRMKSLIMANSYTVSVKHP-ELEGYNALARFE 726
 365 RAFIDPLGIDPRFPRYRHVYAFSSHNKKAAGESFPGIYALF--DIESKVDPSKAWGVK 422
 727 RSFLDEAGIPGHEMYKHLIYGPNLRNHS-QLFSPSLDALYGDVFA-----AQKEVR 779

RESULT 12
 E85075
 probable peptidase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: E85075

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: E85075
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-280 <STO>
 A:Cross-references: GB:NC_001268; NID:97267364; PIDN:CAB81137.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4g07670
 A:Map position: 4

Query Match 10.8%; Score 252; DB 2; Length 280;
 Best Local Similarity 45.5%; Pred. No. 1.9e-11;
 Matches 51; Conservative 16; Mismatches 27; Indels 18; Gaps 3;

20 NVGPGFTGNFSTQKVKMHIHSTNEVTRIVNYIGTLRGAVEDPRVYILGHRDQWVFGID 79
 147 DVGPG-PGILNLSYL-----VTKIQNVIGVIEGEEEDPRVYILRNHRDTWTFRAVD 196
 80 POSGAAYVHETVRSF-----GTLKKGMRPRRTILFASWDAEFGILGS 123
 197 PMSGTAIVLMEASKSYLQHTAQRDLQKRGKMPRTIILCNMDAEYGLVSS 248

RESULT 13
 S67153
 probable membrane protein YOR256c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypotheical protein O5330
 C:Species: Saccharomyces cerevisiae
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
 C:Accession: S67153
 R:Jauniaux, J.C.; Poirey, R.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67153
 A:Accession: S67153
 A:Molecule type: DNA
 A:Residues: 1-809 <JAU>
 A:Cross-references: EMBL:Z75164; NID:91420578; PIDN:CAA99478.1; PID:91420579; GSPDB:G
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: MIPS:YOR256c
 A:Cross-references: SGD:S0005782
 A:Map position: 15R
 C:Superfamily: secretory protein SSP134
 C:Keywords: transmembrane protein
 F:126-142/Domain: transmembrane #status predicted <TM>

Query Match 10.3%; Score 240.5; DB 2; Length 809;
 Best Local Similarity 22.4%; Pred. No. 6.4e-10;
 Matches 98; Conservative 78; Mismatches 160; Indels 101; Gaps 19;

47 IYNYIGTLRGAVEDPRVYILGHRDQWVFGIDQSGAAVYHETVRSFGLT-KEGMRPR 105
 423 IPNIYKIEGREGOSKALIIAASRNSINFGTYNPFGTALLISTYOLFQEVKRYFGMKRL 482
 106 RTILFASWDAEFGILGSTEAEONSRLQER-----GVAYINADSSIGCNTYLR 155
 483 RNIVPISFGGTEFNAGSSELYEQRLPLKDEITYSLIDISQIGIFAKYENGKRGELS 542
 156 VCCPTLMTSLVYNLTKEKSDDEGEKSLYESWTKKSPSPF-SGMRIKSLGSGNFE 214
 543 IETHPLLKFF-FNRNAH-GNFDISVDNVOHYGDWF-----PFLANGIP-VSVISSD---- 590
 215 VFQRLIGIASGRARYTKNMTNKGSGYPLYHSVYETIYELVEKFYDP-----MFK 263
 591 -----STRNRDPT-ETSE-----DKFEVERKILEDEONQSVKOLLVYL 629
 264 YHLTVAVQVGVFELANSIVLPFCRDYAVVLRKYADKIYNISKHPOEMKTYSLSPDS 323
 630 LHISM-----ELIDPLLHFIDISTY--VEDIDERLQLEQAVPERK-----LNFTS 672

```
OY 324 LFSAVKNTETLASKFSERLQDF-----DKSNPILLRM---MNDQMLFERAFIDPL 371
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 673 IKGLLEFMKKISEMAWFTQGMENIYWSHGDIIEPLSLINRMTWKKLTLNIGRRICSPA 732
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 372 GPPDRPFYRHVITYAAS-----SHNKYAGE-----SFPCTIYALDIESEKVPSPKAMGVKQ 423
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 733 GLPNRSFYKKNVLFGLTLQEDKSKNGKNGVDFTFPGVDATYDD-----WKRAQEQ 784
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 424 ISVAAFVQAAAEITLSE 440
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 765 IDLIGKVLHQSAALFVE 801

RESULT 14
S65188
secretory protein SSP134 - Yeast (Saccharomyces cerevisiae)
N.Alternate names: protein P2267; protein YPL176c
C.Species: Saccharomyces cerevisiae
C.Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 19-Apr-2002
C.Accession: S65188; JH0485
R.Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansoerge, W.
submitted to the Protein Sequence Database, May 1996
A.Reference number: S65183
A.Accession: S65188
A.Molecule type: DNA
A.Residues: 1-783 <BEN>
A.Cross-references: EMBL:Z73532; NID:q1370370; PIDN:CAA97883.1; PID:q1370371; MIPS:YPL17
A.Experimental source: strain S288C (A9972)
R.Stidnu, R.S.; Mathewes, S.; Bolton, A.P.
Gene 107, 111-118, 1991
A.Title: Selection of protein-encoding genes by fusion with PHO5 in Saccharomy
A.Reference number: JH0483; MUID:92077420; PMID:1743509
A.Accession: JH0485
A.Molecule type: DNA
A.Residues: 66-149, 'P', 151-318, 'R', 320-414 <SID>
A.Note: the authors claim that sequence of residues 41-57 is signal sequence
A.Note: the authors translated the codon TTA for residue 34 as Phe, GAT for residue 201
C.Genetics:
A.Gene: SSP134
A.Cross-references: SGD:S0006097
A.Map position: 16L
C.Superfamily: secretory protein SSP134
C.Keywords: glycoprotein
F.139, 213/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.7%; Score 179.5; DB 2; Length 783;
Best Local Similarity 19.7%; Pred. No. 2.3e-05;
Matches 93; Conservative 82; Mismatches 169; Indels 127; Gaps 20;

OY 15 LKSYNVGPGFTGNFSTOKVKMHIST-NEVTRIVNIGTLRGAVPEPDRIYILGHRDSM 73
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 374 VAFSNNL---FSGSLNDCLDLIVQTAERHPVDIVKIEGSEDAQAIIYIAAFRNSA 430
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 74 VEGGIDPOSGAAVHETVRSFGLT-KKEGMRPRRTILFASMDAEFGLLGSTEWADNSR 132
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 431 SYGTWMPSPRGTVLLSLDLYOEMVKKFPMKPLRNIFYISFGSEFENAGATEIMEKRE 490
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 133 LQERGVANINA-----DSSIEGNYTLRVCTPLMISLVNLTRELKSPDEGFGRKL 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 491 ALKSEIYTIIDVGQIGIMDSN---NEIQCHPLVDL---FOKNMRSRKNVAVDV 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 186 YE-SWTKKSPSPERS-GMP-RISKLGSNDFEVFF---ORLGIASGRARTKNETNK 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 543 HQPGDWI-----PYLAGQIPVALISPGVMNREHPRIYIYEDKFDLKLRKKKGEV--- 595
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 238 FSGYPLYSVSYETVELVEKFDPMKRYHLTVAVQKGMVFEANSLIVLPDCRDYAVLR 297
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 596 LSEIMLY-----LVKK-----SLELIDPEIPFSISNYVDFL- 627
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 298 KYADKIYNISMKHPQEMKYYISLSPDSLFSAVKNFTETLASKFSERLQDFPKSNPILLRMN 357
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 628 -----STTLKDLQKCPDVIYNFDEVFLGTILMENTKLQFEKMSW----- 668
```

```
OY 358 DQIMFLERAFIDPL-----GLPDRPFYRHVITYAASSHNKA 393
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 669 TELMWAGATYIEPTLAINRMWSNVLISLGVYQCLEGIMDRTEFKNVIFGFKLM----- 724
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 394 GESFPGIYALDIESEKVPSPKAM--GDYKROIISNAF--TVQAAATLSEV 441
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 725 -----VDKGDPLRSWTFPEIRDIATIKDWSVQVQANTLGTI 761
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
G82759
hypothetical protein XF0820 [imported] - Xylella fastidiosa (strain 9a5c)
C.Species: Xylella fastidiosa
C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C.Accession: G82759
R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A.Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A.Reference number: A82515; MUID:20365717; PMID:10910347
A.Note: for a complete list of authors see reference number A59328 below
A.Accession: G82759
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-529 <SIM>
A.Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83630.1; GSPDB:GN
A.Experimental source: strain 9a5c
R.Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Bionex, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neiro, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rose, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A.Reference number: A59328
A.Contents: annotation
C.Genetics:
A.Gene: XF0820
C.Superfamily: Xylella fastidiosa hypothetical protein XF0820

Query Match 7.4%; Score 173; DB 2; Length 529;
Best Local Similarity 31.1%; Pred. No. 4e-05;
Matches 66; Conservative 30; Mismatches 70; Indels 46; Gaps 11;

OY 42 NEVTRIVNIGTLRGAVPEPDRIYILGHRD-----SWVF-GGIDPOSGAAVHE 89
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 270 SEVITSHNVAARLQCAHDEVIYISAHMDHLGVGAPDAKGDITIFGALDMSGTAALE 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 90 TVRSFGLTKEGMRPRRTILFASMDAEFGLLGSTEWADNSRLQERGVAINAD----- 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 330 LARGFA-----RGQPORSVLAFLAVTAEEKGLGS-eyvasnplyrpektvavavnmvmp 384
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 146 -----SSIEGNY-FLRVCTPLM-----YSLVNLITRELKSPDEGFGRKSLYESWTKKSPS 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 385 QGFTRDFGTYGTAKLDDLMLKOVAAAGMKRLRYTLD---PTEAGHFRSDHFSFAKR--- 438
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 196 PEFSGMRISKLGSNDFEVFFQRLGIASGRA 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 439 -----GIPALS-YSAQGDMEVG-----GVAAGKA 461
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: October 4, 2003, 23:26:01
Job time : 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2003, 23:00:27 : Search time 77 Seconds
(without alignments)
1481.289 Million cell updates/sec

Title: US-09-973-382C-2
Perfect score: 2329
Sequence: 1 MGSAPDPSWRSGLKVSYN.....QISVAFTVQAALTLSEVA 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2329	100.0	442	4 Q9HBA9	Q9HBA9 homo sapien
2	2097.5	90.1	719	4 Q8TAY3	Q8TAY3 homo sapien
3	571.5	24.5	614	16 Q8PGK5	Q8PGK5 xanthomonas
4	545.5	23.4	1483	5 Q93332	Q93332 caenorhabdit
5	415.5	17.8	768	6 Q8H2V3	Q8H2V3 sus scrofa
6	412	17.7	621	10 Q94JH4	Q94JH4 oryza sativ
7	404.5	17.4	298	10 Q8LQ61	Q8LQ61 oryza sativ
8	353.5	13.2	606	10 Q94JH3	Q94JH3 oryza sativ
9	252	10.8	280	10 Q9XH28	Q9XH28 arabidopsis
10	240.5	10.3	809	3 Q08693	Q08693 saccharomyc
11	224.5	9.6	515	11 Q8C872	Q8C872 mus musculu
12	179.5	7.7	783	3 Q08919	Q08919 saccharomyc
13	173	7.4	529	16 Q9PF58	Q9PF58 xylella fas
14	158	6.8	549	16 Q8P530	Q8P530 xanthomonas
15	157	6.7	467	16 Q9A5A8	Q9A5A8 caulobacter
16	156	6.7	549	16 Q8PP50	Q8PP50 xanthomonas

17	152.5	6.5	430	16 Q9A3U5	Q9A3U5 caulobacter
18	151	6.5	414	16 Q8EBH7	Q8EBH7 shewanella
19	149	6.4	501	2 P96152	P96152 vibrio chol
20	148	6.4	501	16 Q9KID3	Q9KID3 vibrio chol
21	146.5	6.3	375	16 Q8P625	Q8P625 xanthomonas
22	146.5	6.3	536	16 Q8P326	Q8P326 xanthomonas
23	144.5	6.2	449	2 Q93EJ5	Q93EJ5 bacillus 11
24	142.5	6.1	472	16 Q8PHE8	Q8PHE8 xanthomonas
25	139.5	6.0	393	2 Q82996	Q82996 aeromonas p
26	138	5.9	1066	16 Q8CK35	Q8CK35 streptomyc
27	137.5	5.9	337	17 Q8TY04	Q8TY04 methanopyru
28	136	5.8	470	11 Q9WVJ3	Q9WVJ3 mus musculu
29	133.5	5.7	536	16 Q8PFH7	Q8PFH7 xanthomonas
30	133	5.7	374	3 Q04033	Q04033 saccharomyc
31	131	5.6	472	11 Q9TIV0	Q9TIV0 rattus norv
32	131	5.6	472	11 Q921Y1	Q921Y1 rattus norv
33	130.5	5.6	500	16 P96264	P96264 mycobacteri
34	128.5	5.5	522	16 Q8ED13	Q8ED13 shewanella
35	126.5	5.4	493	5 Q76552	Q76552 acanthocheil
36	126	5.4	485	2 Q53737	Q53737 streptomyc
37	122.5	5.3	472	4 Q8NB21	Q8NB21 homo sapien
38	122.5	5.3	472	4 Q9T646	Q9T646 homo sapien
39	122.5	5.3	541	4 Q9Y5X6	Q9Y5X6 homo sapien
40	121.5	5.2	536	16 Q9HZ08	Q9HZ08 pseudomonas
41	121	5.2	598	16 Q8PRD7	Q8PRD7 xanthomonas
42	120.5	5.2	324	16 Q9F2X2	Q9F2X2 streptomyc
43	120	5.2	506	16 Q8EP07	Q8EP07 shewanella
44	120	5.2	594	16 Q8PER6	Q8PER6 xanthomonas
45	117	5.0	609	2 Q8VUS4	Q8VUS4 alteromonas

ALIGNMENTS

RESULT 1
Q9HBA9 PRELIMINARY; PRT; 442 AA.
AC Q9HBA9:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT Prostate-specific membrane antigen-like protein.
GN PSMA/SCP III.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA O'Keefe D.S., Bacich D.J., Heston W.D.W.;
RT "Expression Profile of Prostate-Specific Membrane Antigen (PSMA)
RT versus a Prostate-Specific Membrane Antigen-Like Gene in Normal
RT Tissues, Prostate Cancer and Tumor Associated-Vasculature.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA O'Keefe D.S., Bacich D.J., Heston W.D.W.;
RT "Cloning and Characterization of a novel glutamate-preferring
RT peptidase that maps to the SCZDI1 locus: a candidate gene for
RT Schizophrenia?";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF261715; AAG29102.1; -
DR Pfam; PF04253; TFR_dimer; 1.
SQ SEQUENCE 442 AA: 50044 MW: 26CD6E082AC1E8D3 CRC64;
Query Match 100.0%; Score 2329; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.6e-170;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSAPDPSWRSGLKVSYNPGFTGNFSTQKVKMHIHSTNEVRIYVIGTLGAAVEP 60
|||||

```
Db 1 MGSAAPPDSSSRGSLKSYNVNGPGFTGNFSTOKYKMHISTNEVTRIVNIGTLRGAVEP 60
QY 61 DRYVILGGHRDSWFGGIDPOSGAAVHETVRSFGLTKEGMRPRRTILFASWDAEEFGL 120
Db 61 DRYVILGGHRDSWFGGIDPOSGAAVHETVRSFGLTKEGMRPRRTILFASWDAEEFGL 120
QY 121 LGSFEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
Db 121 LGSFEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
QY 121 LGSFEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
Db 121 LGSFEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
QY 181 ECKSLYESWTKKSPSPFSGMRPRISKLSGNDPEFFFORLGIASGRARYTKNMETNKFSG 240
Db 181 ECKSLYESWTKKSPSPFSGMRPRISKLSGNDPEFFFORLGIASGRARYTKNMETNKFSG 240
QY 181 ECKSLYESWTKKSPSPFSGMRPRISKLSGNDPEFFFORLGIASGRARYTKNMETNKFSG 240
Db 181 ECKSLYESWTKKSPSPFSGMRPRISKLSGNDPEFFFORLGIASGRARYTKNMETNKFSG 240
QY 241 YPLXHSYETVELVEKFEYDPMFKYHLTVAQYRGGMVELANSIYLPDPCRDYAVVLKRYA 300
Db 241 YPLXHSYETVELVEKFEYDPMFKYHLTVAQYRGGMVELANSIYLPDPCRDYAVVLKRYA 300
QY 301 DKIVNISMKHPOEKKTYSLSFSDSLFSAVKNFETLASKFSERLQDFDKSNPILLRMMNDOL 360
Db 301 DKIVNISMKHPOEKKTYSLSFSDSLFSAVKNFETLASKFSERLQDFDKSNPILLRMMNDOL 360
QY 301 DKIVNISMKHPOEKKTYSLSFSDSLFSAVKNFETLASKFSERLQDFDKSNPILLRMMNDOL 360
Db 301 DKIVNISMKHPOEKKTYSLSFSDSLFSAVKNFETLASKFSERLQDFDKSNPILLRMMNDOL 360
QY 361 MFLERAFIDPLGLDPRPPYRHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 420
Db 361 MFLERAFIDPLGLDPRPPYRHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 420
QY 421 KROIISVAAFVQAAAEETLSEVA 442
Db 421 KROIISVAAFVQAAAEETLSEVA 442
```

RESULT 2

```
OC 08TAY3 PRELIMINARY; PRT: 719 AA.
AC 08TAY3:
DT 01-JUN-2002 (TREMblrel. 21, Created).
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Similar to folate hydrolase (Prostate-specific membrane antigen)
DS 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC025672; AAR25672.1; -.
DR InterPro; IPR003137; PA.
DR Pfam; PF04225; PA; 1.
DR Pfam; PF04253; TFR_dimer; 1.
DR PROSITE; PSS0840; PA; 1.
KW Hydrolase.
SQ SEQUENCE 719 AA; 80597 MW; AF79A10CA2BF9DF4 CRC64;
```

Query Match 90.1%; Score 2097.5; DB 4; Length 719;
Best Local Similarity 91.0%; Pred. No. 1.9e-152;
Matches 402; Conservative 6; Mismatches 3; Indels 31; Gaps 1;

```
QY 1 MGSAAPPDSSSRGSLKSYNVNGPGFTGNFSTOKYKMHISTNEVTRIVNIGTLRGAVEP 60
Db 309 MGSAAPPDSSSRGSLKSYNVNGPGFTGNFSTOKYKMHISTNEVTRIVNIGTLRGAVEP 368
QY 61 DRYVILGGHRDSWFGGIDPOSGAAVHETVRSFGLTKEGMRPRRTILFASWDAEEFGL 120
Db 369 DRYVILGGHRDSWFGGIDPOSGAAVHETVRSFGLTKEGMRPRRTILFASWDAEEFGL 428
QY 121 LGSFEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
Db 429 LGSFEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 488
```

```
QY 181 ECKSLYESWTKKSPSPFSGMRPRISKLSGNDPEFFFORLGIASGRARYTKNMETNKFSG 240
Db 489 ECKSLYESWTKKSPSPFSGMRPRISKLSGNDPEFFFORLGIASGRARYTKNMETNKFSG 548
QY 241 YPLXHSYETVELVEKFEYDPMFKYHLTVAQYRGGMVELANSIYLPDPCRDYAVVLKRYA 300
Db 549 YPLXHSYETVELVEKFEYDPMFKYHLTVAQYRGGMVELANSIYLPDPCRDYAVVLKRYA 608
QY 301 DKIVNISMKHPOEKKTYSLSFSDSLFSAVKNFETLASKFSERLQDFDKSNPILLRMMNDOL 360
Db 609 DKIVNISMKHPOEKKTYSLSFSDSLFSAVKNFETLASKFSERLQDFDKSNPILLRMMNDOL 656
QY 361 MFLERAFIDPLGLDPRPPYRHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 420
Db 657 -----KHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 697
QY 421 KROIISVAAFVQAAAEETLSEVA 442
Db 698 KROIISVAAFVQAAAEETLSEVA 719
```

RESULT 3

```
OC 08PGK5 PRELIMINARY; PRT: 614 AA.
AC 08PGK5:
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Peptidase.
GN XAC3611.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Queglio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cammanan F., Cardozo J., Chambergro F., Ciapina L.P.,
RA Ciarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A.F., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012011; AAM38454.1; -.
DR Pfam; PF04253; TFR_dimer; 1.
KW Complete proteome.
SQ SEQUENCE 614 AA; 66255 MW; 636C3FE15BF008DD CRC64;
```

Query Match 24.5%; Score 571.5; DB 16; Length 614;
Best Local Similarity 30.5%; Pred. No. 2.3e-35;
Matches 148; Conservative 78; Mismatches 176; Indels 83; Gaps 13;

```
QY 1 MGSAAPPDSSSRGSLKSYNVNGPGFTGNFSTOKYKMHISTNE-VTRIVNIGTLRGAVEP 58
Db 145 LGGVADE-DWRGALPTTFRIG-----GDARARVHLKVDADWGSCQTIVNATATLKGSE 196
QY 59 EPDRYVILGGHRDSWFGGIDPOSGAAVHETVRSFGLTKEGMRPRRTILFASWDAEEF 118
Db 197 YPDQWVYRGHNRDQWVGADADPLSGTTALLAEAKAIGELAKGQORPARKTIVYASWGDGEA 256
```

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QY 119 GLGSGTEWAEDMSRLLOERGVAIYNADSIEGNTTLRNDICPLMYSLYVNLUTELKSPDE 178
    ||||| ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 GLLGSTEWAEQHADELRRKRAVLYNTDGN--GRGFLNAGGSHALQRLYNSVADVPDPS 314
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 GFE-----GKSLYESTWTKKSPSPESFGMGRISLGSNDVEFEVFORLG 221
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 315 GYSVLERQARARIDALAPAAKPAOKDIAKTAAG---GGDIPLKALSSGSDSYEPLOHIG 371
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 IASGRARYTKMETNKFSGYPLHYSVETVELVERFYDPMFKYHLIYVAQVGGVAFELAN 281
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 372 LATLDLGY-----GGQGGSGGYVSHLYDSYDYFARFIIDPGFAYPLILSQYVGRVLVAN 426
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 SYLVPDCCDIAVYLARKYADKIYINISMKHPDEMKTYIS--LSDSLSFSKVN----- 330
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 427 APVLPORFEGFDAVAGYAQELKQOAPDSRTAARTQOELLQAGAYAAVDNPNRPORAPED 486
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 331 -----PTELASKFSERLDPDFKSNPIL-----RMNDOLMPLERAFIDP 370
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 487 KAAVPOIDFALDOAIIT--RLDSSAKRYMAMALAANGNIDAHVNSKLKLAISQRIODYTLLAE 545
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 371 LGLIPRPFYRHVITYAPSSHNKYAGESPGIDALDEJESKVPDSKAMGVKROIISVAAPT 430
    ||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 546 AGLPGRPFYRNLITYAPGLATGYEVVTLFGIREALED-----RRNEDLSRTI----- 591
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 431 VQAAA 435
    || ||
Db 592 VQTAA 596

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RESULT 4
Q93332
ID Q93332
PRELIMINARY;
PRT: 1483 AA.

DT	01-FEB-1997 (TREMBLrel. 02, Created)	
DT	01-FEB-1997 (TREMBLrel. 02, last sequence update)	
DT	01-MAR-2003 (TREMBLrel. 23, last annotation update)	
DE	C35C5.2 protein.	
GN	C35C5.2	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Ploiderinae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
PN	[1]	
RP	SEQUENCE FROM N.A.	
RA	White S.;	
RL	Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=99069613; PubMed=9851916;	
RA	none;	
RT	"Genome sequence of the nematode C.elegans: A platform for	
RT	investigating biology."	
RL	Science 282:2012-2018(1998).	
DR	EMBL; Z78417; CAB01688.1; -.	
DR	MEROPS; M28.011; -.	
DR	WormPep; C35C5.2; CE08584.	
DR	InterPro; IPR003137; PA.	
DR	Pfam; PF02225; PA; 2.	
DR	Pfam; PF04253; TFR_dimer; 2.	
DR	PROSITE; PS50840; PA; 2.	
DR	SEQUENCE 1483 AA; 168164 MW; AE07537AD5E86FEC CRC64;	
Query Match	23.4%;	Score 545.5; DB 5; Length 1483;
Best Local Similarity	31.1%;	Pred. No. 8.5e-33;
Matches 147; Conservative	84;	Mismatches 181; Indels 61; Gaps 16

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Query Match 23.4% Score 545.5; DB 5, Length 1483;
Best Local Similarity 31.1%; Pred. No. 8, 5e-33;
Matches 147; Conservative 84; Mismatches 181; Indels 61; Gaps 16

QY 1 MCGSAPDDSSWFGSLKSYINWPGFTGTFSTQYKKMHISTNE-----V 44
    :::::..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:
DB 320 MCGDA-VNADFGKLNLYRPGGLINN--ÖKLNLYVHENERSVYVELISRLT 375
    :::::..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:

QY 45 TRIYNYIGLRAVEPDRYVILGGHRDSWVGEGIDPQSGAAVHETRSFGTLKKE-GWR 103
    :::::..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:
QY 376 RRIQNIIMGKIKSQDPKDFVLSNINMIDMTGAVDPMSGTSTLEESRALKROYONOTGW 435
    :::::..:..:..:..:..:..:..:..:..:..:..:..:..:..:..:

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[illegible]

RESULT 5	
Q8H2V3	
ID Q8H2V3	PRELIMINARY;
	PRT; 768 AA.

DT 01-MAR-2003 (TEMBREL. 23, Created)
DT 01-MAR-2003 (TEMBREL. 23, Last sequence update)
DT 01-MAR-2003 (TEMBREL. 23, Last annotation update)
DE Transferrin receptor.
GN TRC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RC TRISSE-Small intestine;
RA Pithon P., Jorg H., Neuenchwander S., Stranzinger G., Vogel P.,
RT "The complete cDNA sequence of porcine transferrin receptor gene.",
RL submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF016763; AAN09749.1; -.
KW Receptor.
KW SEQUENCE 768 AA; 86121 MW; 55B15CEFA2F4D1CF CRC64;

Query Match	17.8%;	Score 415.5;	DB 6;	Length 768;
Best Local Similarity	24.7%;	Pred. No. 3.1e-23;		
Matches 112;	Conservative 90;	Mismatches 169;	Indels 83;	Gaps 12

[illegible]

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OY 292 YAVLRKYADKIYNISMKHPQ---EMKTYISLSPDLSFAVKNFTIASKFSRLDOPDKS 348
DB 619 -----YEMINDILSLVREMNQPRVDIREMGLSLQWLYSARGDEFFRATSRILSDYNNVETR 674
OY 349 NPILRMNNDOLMFLERAFIDPLGLPDRPFYRHVYAPSSHNNKYAGESFPGLYDALPDI-I 407
DB 675 DKFVREIRIDRMKEVYHFLSPYSPRESPPRHITWGSQSHI-----LSALVEHL 724
OY 408 ESKVDPSKMGD--VKROIISVAALFTVQAAETLS 439
DB 725 KLRKNSSAFNQTLKNOALATATWTIOGAANALIS 758

RESULT 6
OY 094JH4 PRELIMINARY; PRT; 621 AA.
ID 094JH4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Peptidase-like protein.
GN P0638D12.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GN3) genomic DNA, chromosome 1, PAC
clone:p0638D12.15"
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002972; BAB55507.1; -.
DR Gramene; O94JH4; -.
DR InterPro; IPR003137; PA.
DR Pfam; PF02325; PA. 1.
DR Pfam; PF04253; TPR_dimer; 1.
DR PROSITE; PS50840; PA. 1.
DR SEQUENCE 621 AA; 67139 MW; 8D471DA2259016A4 CRC64;

Query Match 17.7%; Score 412; DB 10; Length 621;
Best Local Similarity 24.2%; Pred. No. 4.2e-23;
Matches 111; Conservative 63; Mismatches 116; Indels 168; Gaps 12;
OY 1 MGSAPPDSSWRG-SLKVSYNWGPG-----FTGNSTQVKKMHISTNEVTRIYVIG 52
DB 309 LGGDAAP-ADMQREGSPVYRLGPPAILNLTYGN-----DMATLENVFA 354
OY 53 TLKRAVEDPRVILIGHRDWNFGCIDPQSGAAVYHETVNSFGTLKKGKGRPRRTILFAS 112
DB 355 VIEEAEEPRDRIIVLIGNRDAMTFGASDPNSGTAAMIEAQLSLVLRQKGRPRRTIIFCS 414
OY 113 WDAEEFGILGSTEWAEDNSRLQERGVAIYIADSSIGNTLARDCTPIIMSLYNNLKE 172
DB 415 WDAEEYGL----- 422
OY 173 LKSPDEGFEKSLYESWTKRSPSPFGSMPRISKLGSGNDFEYFORLIASGRARYTK- 231
DB 423 VQPDND--SSQAVYDSWVKSNIPLDQAIPII-----IRYTM 458
OY 232 --AMETKKSFGSYPLIYHSHVETVELVEKFTYDPMFKYHLTVAQVRGWNVELANSIVLPDC 289
DB 459 SCGRNNEIIG----- 469
OY 290 RDYAVVLRKYADKIYNISMKHPQEMKTYISLSPDLSFAVKNFTIASKFSRLDOPDI--- 346
DB 470 --SVGTLOANTTKYVEN-----EVKGTALSCSPFLHNAIRALKTAARKVNGEREIOLROL 520
OY 347 -----KSNPILRMNNDOLMFLERAFIDPLGLPDRPFYRHVYAPSSHNNKYAGESFPGLY 401
DB 521 SSNQLKKDSMKIRSLNRLMQAERAFINRBSGLFKREMFKHLIVYGPSEQNDMESASTYGEV 580
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OY 402 DALFDIESKVDPSKMGDVKKROIISVAALFTVQAAETLS 439
DB 581 NAIASAR-KENTTESMKRFVQEHHRVARATIQASVILA 617

RESULT 7
OY 08LO61 PRELIMINARY; PRT; 298 AA.
ID 08LO61;
AC 08LO61;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative peptidase-like protein.
GN P0439E07.19.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (Japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:p0439E07.19"
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003768; BAB91937.1; -.
DR Gramene; Q8LO61; -.
DR SEQUENCE 298 AA; 33607 MW; 5051AC9AC9C5BD3 CRC64;

Query Match 17.4%; Score 404.5; DB 10; Length 298;
Best Local Similarity 30.6%; Pred. No. 5.4e-23;
Matches 101; Conservative 69; Mismatches 111; Indels 49; Gaps 9;
OY 121 LGSTEWAEDNSRLQERGVAIYIADSSIEGNTLRVCTPIIMSLYNNLKELSPEEGF 180
DB 3 VGSTEWEEENKAMLTSTRVAYLVNDSAVYG-AGFYASATPOLDELLKEASKOVONPN-- 59
OY 181 EGSLSYESTWTKRSPSPFGSGPRISKL-GSGNDFEYFORLIASGRARYTKMETKFS 239
DB 60 ETQSLYDLDM-----ASDSSSMIKRIGRIGGGSQDSAVQNHIGPS-----IDISMG 107
OY 240 GYPLIYHSHVETVELVEKFTYDPMFKYHLTVAQVRGWNVELANSIVLPDCRDYAVVLRKY 299
DB 108 EYAVYHSLYDDEFVWMEKFCPLFRRHVAASMGVLALRLSDEEILDFPNYSTYAAVELEKG 167
OY 300 ADKIYNISMKHP-----QEMKTYISLSPDLSFAVKNFTIASKFSERLDDPKSN 349
DB 168 AIDINKRLGLVPYSSSPLOKSIAEFKRAALQOMSEMKALQ-----TRKVNPNWRNN 218
OY 350 PILLRMNNDOLMFLERAFIDPLGLPDRPFYRHVYAPSSHNNKYAGESFPGLYDALPDI 409
DB 219 PLKRVOLNEBLMTERAFITREGISGRPWYKHLVY-----PGVDAL- QMAE 264
OY 410 KVDPKAMGDVKKROIISVAALFTVQAAETLS 439
DB 265 RTNTESEWSRSVQEHRIYIARVINOASVLS 294

RESULT 8
OY 094JH3 PRELIMINARY; PRT; 606 AA.
ID 094JH3;
AC 094JH3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Peptidase-like protein.
GN P0638D12.16.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
```

Ox	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Nipponbare;
RA	Sasaki T., Matsumoto T., Yamamoto K.;
RT	"Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 1, PAC
RL	clone:p0638D12."
DR	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AP002972; BAB55508.1; -
DR	Graeme; Q94JH3; -
DR	InterPro; IPR003137; PA.
DR	Pfam; PF02225; PA; 1.
DR	Pfam; PF04253; TFR dimer; 1.
DR	PROSITE; PS50840; PA; 1
SO	SEQUENCE 606 AA; 65594 MW; F80DDCBF731058B6 CRC64;
Query Match	15.2%; Score 353.5; DB 10; Length 606;
Best Local Similarity	22.4%; Pred. No. 1,3e-18;
Matches	100; Conservative 47; Mismatches 82; Indels 217; Gaps 10
Oy	1 MGSAAPPSSNRGSLKV-SYVNGPG-----FTGNFSTQVKMHINSTEYTRIYNIG 52
Dd	321 MGGAAP-TWOGEGAPMYRILGCPAVALNTLTIGN-----DLTATLENFA 366
Oy	53 TLRGAVEPDRVIIIGHRDMSVFGEIDPOGAAVHYETVRSEGTIKKGMPRRITLLAS 112
Dd	367 VIEKKEEDRVIIIGNHRDAWTFGAVDNSTAAMLEIAERLSKLEKKGWRRPTIIVCS 426
Oy	113 WDAEEFGILGSTWAENDSRLLQERGVAVINADSSIENGYTLRVDCPTLMYSLVYNLRKE 172
Dd	427 WDAAEFPL- 434
Oy	173 LKSPDEGEFKSLYESWTKRSPSEFSGMPRI SKLGNDPEVEFQRLGIASGRARYTKN 232
Dd	435 VOODED-----PS----- 442
Oy	233 WEWKFGSGPIYHSVLEYELVEKFYDPMEFYHLTVAGVREGMFFELANSYLPPDCXDY 292
Dd	443 -----QTLYDTMIMHHPPMLD-----AEKNW 462
Oy	293 AVVRYRKADKIYINISMKHPOEMKYTLSFDLSFSAVNKFTFLASKFSERLDFDKSNIL 352
Dd	463 SLKTRATVAV----- 473
Oy	353 LRMMNDQLMERAFIDLPLGPDRPFYRHVITYAESHNKYGESPGIYDALFDIESKVD 412
Dd	474 -RDINDRLMAAERGEFINREGIDGSPWVKHMIIYASSDDODDMOTKAFPGLVSAL-DKANLN 531
Oy	413 PSKAMGVYKROIISVAFTVOAAETL 438
Dd	532 TTESWOLLQHEIYRAARAVSKASAVL 557
<hr/>	
RESULT 9	
O9XH28	PRELIMINARY; PRT; 280 AA.
O9XH28	AC O9XH28;
DT	01-NOV-1999 (TREMBLrel_12, Created)
DT	01-NOV-1999 (TREMBLrel_12, last sequence update)
DT	01-MAR-2003 (TREMBLrel_23, last annotation update)
DE	F10A2.10 protein (Putative peptidase).
GN	F10A2.10 OR AT4G07670.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosidis II; Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Columbia;
RA	WASHU;
RT	"The A. thaliana Genome Sequencing Project.";
RL	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

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RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia.
RA      Joshi C., Bauer C., Holic M.,
RT      "The sequence of A. thaliana F10A2."
RL      Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia.
RA      Waterston R.
RL      Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia.
RA      Waterston R.
RL      Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia.
RA      Waterston R.
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN      [6]
RP      SEQUENCE FROM N.A.
RC      EU Arabidopsis sequencing project.
RL      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF147259; AAD29787.1; -.
DR      EMBL; AL161506; CAB81137.1; -.
DR      HSSP; P02786; 1CX8.
DR      InterPro; IPR003137; PA.
DR      Pfam; PF02225; PA; 1.
DR      PROSITE; PSS0840; PA; 1.
SQ      SEQUENCE 280 AA; 3115 MW; AB7EFCFAE1870386 CRC64;

Query Match          10.8%; Score 252; DB 10; Length 280;
Best local similarity 45.5%; Pred. No. 2,5e-11;
Matches 51; Conservative 16; Mismatches 27; Indels 18; Gaps 3;

QY      20 NCGPFTGNESTOKVKNHISTNEVTRIVNYIGTLGCAVEPDRYVILGHRDSWVFGCID 79
DB      147 DVGPG-IGIINLXYI-----VTKIQNVIGVIEGEEPPDRYVILNRHDTWTFRAVD 196
QY      80 PQSAANVHVEVRSF-----GLKKEGRPRRTILFASMDAEFGILGS 123
DB      197 PNSTAVLMEKSKSYLQHIAORDLQKRGWKPRTIILCMWADEEYGLVSS 248

RESULT 10
Q08693 PRELIMINARY; PRT; 809 AA.
AC      Q08693;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-MAR-2003 (TREMblrel. 23, annotation update)
DE      Chromosome XV reading frame ORF YOR256C.
GN      YOR256C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RX      NCBL_TaxID=4932;
RP      SEQUENCE FROM N.A.
RA      MIPS;
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97298311; PubMed=9153759;
RA      Sauniaux J.C., Potrey R.;
RT      "Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV
RT      reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1,
RT      RIL2, PNI1, PAC1 and VPH1."
RL      Yeast 13:483-487 (1997).
RL      EMBL; Z75164; CA99478.1; -.
RL      SGD; S0005782; YOR256C.

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DR InterPro: IPR003137; PA.
DR Pfam: PF02225; PA: 1.
DR Pfam: PF04253; TFR_dimer; 1.
DR PROSITE: PS50840; PA: 1.
DR SEQUENCE 809 AA; 91995 MW; D7D68C0A8C50ECB2 CRC64;
Query Match 10.3%; Score 240.5; DB 3; Length 809;
Best Local Similarity 22.4%; Pred. No. 9.2e-10;
Matches 98; Conservative 78; Mismatches 160; Indels 101; Gaps 19;
47 IYNYGTLRGAVPEPRVYILGHRDSWFGIDIPQSGAAVHETVRSFGTLK-KEGMRPR 105
423 IPNIVGKIEGRQSKAKIIIAASRNSINFGTTPNFGAALSIYOLFQEVYKFGKMPDL 482
106 RTILPASPDAEEFGILGSTEMAEDNSRLQER-----GVAYINADSSIEGNTYLR 155
483 RNIVYISGCGTEFNAGSELSIEORLTPLKDEIYSLIDISOLGIPFAEKYENGKTRGELS 542
156 VDCITPLMSLVYNTLRELKSLSPDEGKSLYESWTKKSPSEF-SGMPRIKSLSGNDPE 214
543 IETHPLLKRF-FNRNNAH-GNFIISVDNOHYGDMT-----PFLANGIP-VSYISSD---- 590
215 VEFORLIASGRARYTKNMEYKFSGYPLYSVETVELVEFYDP-----MFK 263
591 -----STNNRDTPT-ETSE-----DKFERVEKILDEQNOQSYKDLLVYL 629
264 YHLYVAOVGKGVFELANSIVLPFCRDYAVYLKRAKTIYNSMKHPQEMKTYSLSPDS 323
630 LHTSM-----ELIDPLLHFDILISY--VEDIDERLQRLQAYPEK-----LNFTS 672
324 LPSAVNPFELISKESERLODF-----DKSNPILRLM--ANDOLFLERAFIDPL 371
673 IIRGLLEFWKIGSEMAWTOGWNENIYWSHODGIEPILSLINRTYKTKLLINIRFCSPA 732
372 GLDPRFPRVHVIYAPS-----SHNKYAGE--SFPGIYDALPDIKSKVDPSKAWGVKQ 423
733 GLPNRSFYKVVLPGLPILOEDKSKGNVDQFMTFPGVMDAIIYDD-----WKRAQEQ 784
424 ISVAALFTVQAALFTLSE 440
785 IDLIGKVLHQSAAFLVE 801
Db
RESULT 11
08C872 PRELIMINARY; PRT; 515 AA.
08C872 AC
01-MAR-2003 (Tremblrel. 23, Created)
01-MAR-2003 (Tremblrel. 23, Last sequence update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Transferin receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA THE FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK048228; BAC33277.1;
SQ SEQUENCE 515 AA; 57341 MW; 86FC77FF66A80DDF CRC64;
Query Match 9.6%; Score 224.5; DB 11; Length 515;
Best Local Similarity 34.6%; Pred. No. 8e-09; Indels 21; Gaps 6;
Matches 55; Conservative 31; Mismatches 52;
1 MGSNAP-----DSSWMSGLKVGYNVNGPFTGNFSTQKVMHISTNEVTRIYNVIGTLRG 56

Db
351 MESSCPARMINDSCK--LELSON-----QNVKLIVKNVLEKERRILNIFGVYNG 397
OY 57 AVEEDRVYILGHRDSWFGIDIPQSGAAVHETVRSFG-FLKKEGMRPRRTILPASN 113
Db 398 YEEDDRVYVVAQDA--LGAGVAARKSSVGTGLTLKLAQVSDMTSKDGFPSRSIIIFASN 456
OY 114 DAEEFGLLGSTEMAEDNSRLQERGVAYINADSSIEGNY 152
Db 457 TAGDGAAGATEMLEGYLSSHLKAFYIINDKYYLKGK 495
Db
RESULT 12
008919 PRELIMINARY; PRT; 783 AA.
ID 008919
AC 008919;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Chromosome XVI reading frame ORF YPL176C.
GN YPL176C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Nentwich U., Voss H., Ansgore W.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS: Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
RL EMBL: Z73532; CAAG7883.1;
DR SGD: S0006097; YPL176C.
DR InterPro: IPR003137; PA.
DR Pfam: PF02225; PA: 1.
DR Pfam: PF04253; TFR_dimer; 1.
DR PROSITE: PS50840; PA: 1.
SQ SEQUENCE 783 AA; 88735 MW; 85D78D5D2FEL1A47 CRC64;
Query Match 7.7%; Score 179.5; DB 3; Length 783;
Best Local Similarity 19.7%; Pred. No. 4.2e-05;
Matches 93; Conservative 82; Mismatches 169; Indels 127; Gaps 20;
OY 15 LKSYNVNGPFTGNFSTQKVMHIST-NEVTRIYNVIGTLRGAVPEPRVYILGHRDSW 73
Db 374 VKFSNLT---FSGSLNDCRLDLVQTAIRERHPVHDVIGKIEGSEQAGRAIVLAAPNSA 430
OY 74 VFGIDIPQSGAAVHETVRSFGTL-KEGMRPRRTILPASPDAEEFGILGSTEMAEDNSR 132
Db 431 SYGTWPSFGIVVLLSLIQLQEVNYKFDMPKLNKIFISFGSEFENAGATELMEKRT 490
OY 133 LQERGVAYINA-----DSSIEGNTYLRVCTPLMKSLVYNTLRELKSLSPDEGFEKSL 185
Db 491 ALKSEIYTIIDVGIGIDMSN-----NLEIQCHPLLVLDL--FQKMTSKSENVKVDNV 542
OY 186 YE--SWTKKSPSPES-GMP--RISKLSGNDPEVF--ORLGIASGRARYTKNMETNK 237
Db 543 HQFGWMT-----PYLAQIPVAILISSPCVMNREHPYIYVEKFPFIDKLADKKKGEV-- 595
OY 238 FSGYPLYSVETVELVEKFPDPMKYHLITVAQVKGAVFELANSIVLPFCRDYAVYLR 297
Db 596 LSEIMLY-----LVK-----SLDLIDDPFIPFISINVDL- 627
OY 298 KYADKIYNSMKHPQEMKTYSLSPDSLFSAVKNFTLASKSERLODFKSNPILLRMN 357
Db 628 -----STLKLQDKCEPDVYNFEVFLGTTLWENTKLOPEKMKSEW----- 668
OY 358 DQMLFLERAFIDPL-----GLDPRFPRVHVIYAPS SHNKYA 393
Db 669 TELMTGAGTYIEPTIIAIIINRSMWYLLSLIGVTOCLEGLEDLDRFTYKKNVITGPKIM----- 724
OY 394 GESPGIYDALPDIKSKVDPSKAW--GDVKKQISVAALFTVQAALFTLSEV 441

Db 725 -----VDKGDPLRSWTFPEIRDTIAIKDMSVQVQANTLGTI 761

RESULT 13

09PF58 PRELIMINARY; PRT; 529 AA.

AC 09PF58; 09PF58;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)

DE Hypothetical protein Xf0820.

GN Xf0820.

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.

OX NCBI_TaxID=2371;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=9a5c;

RA MEDLINE=20365717; PubMed=10910347;

RA SImson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alverenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Boye J.M., Brites M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H., Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., France S.C., Franco M.C., Fromme M., Furlan L.R., Gariel M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P., Krüger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.S., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B.N., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miraca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidants J., Setubal J.C.;

RA "The genome sequence of the plant pathogen *Xylella fastidiosa*," Nature 406:151-159(2000).

RL EMBL: AE003921; AAF83630.1; -

DR InterPro: IPR000010; Cysstatin.

KW PROSITE: PS00287; Cysstatin; 1.

KW Hypothetical protein: Complete proteome.

SQ SEQUENCE 529 AA; 57664 MW; 37EFC71953B41655 CRC64;

Query Match 7.4%; Score 173; DB 16; Length 529;

Best Local Similarity 31.1%; Pred. No. 7.5e-05;

Matches 66; Conservative 30; Mismatches 70; Indels 46; Gaps 11;

QY 42 NEYTRLYNVIGTLRGAVPEDRYVILGGH-----SNWF-GGIDPOSGAAVHE 89

DB 270 SEYITSHNVAAALOGCAHPDETVIYSAHMDHIGVGPADAKGTIFENGALDMSGTAALLE 329

QY 90 TVRSFGTLKKEGMRPRTILFASMDAEEFGILGSTPMADNSRLQERVAIYNAD---- 145

DB 330 LARGFA-----KGPQPORSVFLAVTAEEGGLGS--EYVSNPLVPLEKTVAAVINMDVNP 384

QY 146 ---SSIEGNY-ILRVDCPTLM-----YSLVNYLTKELKSPDEGFGKSLYSWTKKSPS 195

DB 385 QGPTDFGIYGTAKLDLMDLKVAAAGWKLRYTLD---PTPEAGHFRSDHRSFAAR---- 438

QY 196 PEPGMPRIKSLGSGNDFEVFFQRLGIASGRA 227

Db 439 -----GIPALS-YSGODMEVG-----GVAAGKA 461

RESULT 14

08P530 PRELIMINARY; PRT; 549 AA.

AC 08P530; 08P530;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)

DE Aminoepetidase.

GN XCC3517.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RA MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidants J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spínola L.A.F., Takita M., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitaajima J.P.;

RA "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities," Nature 417:459-463(2002).

RL EMBL: AE012471; AAM42787.1; -

KW Complete proteome.

SQ SEQUENCE 549 AA; 59295 MW; B6FB8307A172C071 CRC64;

Query Match 6.8%; Score 158; DB 16; Length 549;

Best Local Similarity 26.2%; Pred. No. 0.0011;

Matches 59; Conservative 33; Mismatches 61; Indels 72; Gaps 10;

QY 42 NEYTRLYNVIGTLRGAVPEDRYVILGGH-----RDSNWF-GGIDPOSGAAVHE 89

DB 291 SPVITSHNVAAALOGCAHPDETVIYSAHMDHIGVGPADAKGTIFENGALDMSGTAALLE 350

QY 90 TVRSFGTLKKEGMRPRTILFASMDAEEFGILGSTPMADNSRLQERVAIYNAD-- 145

DB 351 LARGFA-----KGPKEPRSVFLAVTAEEGGLGSEFYA---SKPLPLATTVAAVINMDGM 403

QY 146 ---SSIEGNY-ILRVDCPTLM-----YSLVNYLTKELKSPDEGFGK 182

DB 404 NPFVPSRDGIYGTAKLELLDQLKTVAGQWKLRYTPD-----KPEAGYTF 449

QY 183 KSLYESWTKKSPSPERSGMPRIKSLGSGNDFEVFFQRLGIASGRA 227

DB 450 RSDHFSFAAR-----GVPAALS-YAAGODMEVG-----GVAAGKA 482

RESULT 15

09A5A8 PRELIMINARY; PRT; 467 AA.

AC 09A5A8; 09A5A8;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)

DE Aminoepetidase, putative.

GN CC2544.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernmen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005922; AAK24515.1; -.
DR TIGR: CC2544; -.
DR InterPro: IPR003137; PA.
DR PROSITE: PS50840; PA: 1.
KW Complete proteome.
SQ SEQUENCE 467 AA; 48918 MW; 9984DE2A9D84F00F CRC64;

Query Match 6.7%; Score 157; DB 16; Length 467;
Best Local Similarity 30.3%; Pred. No. 0.0011;
Matches 44; Conservative 28; Mismatches 59; Indels 14; Gaps 6;
OY 30 STOKVKMHI-----HSTNEVTRIVNIGTLRGAVEPDRVILGGHDSWVF--GGIDPQS 82
DB 232 AARKVPRVKLKLESSVNPNNVAMNISGDIGSEKPDDEVIVIGGHLDSWDVGTGALDDAT 291
OY 83 GAAVVEHTVRSFGTLKKKGWRPRRTILFASWDAEFGILGSTE-WAEDNSRLLOERGVAY 141
DB 292 GIATTTAAKLIQDLPK--RPKRTIRVVMWGSESG--GSSEAYLAANKDALSTMVLG 346
OY 142 INADSSIEGNTLRVDCPLMYSLV 166
DB 347 -ESDPTGADRIYSIQVPAAGSLDHPV 370

Search completed: October 4, 2003, 23:25:13
Job time : 81 secs